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OM nucleic - nucleic search, using sw model

Run on: April 11, 2005, 19:46:51 ; Search time 4.05825 seconds  
(without alignments)  
7660.750 Million cell updates/sec

Title: US-09-979-558A-2

Perfect score: 19

Sequence: 1 taatgtcatcgtcccccggg 19

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents NA:\*
- 1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq:\*
  - 2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq:\*
  - 3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq:\*
  - 4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq:\*
  - 5: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq:\*
  - 6: /cgn2\_6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	16.4	86.3	2132	3	US-09-552-322-1 Sequence 1, Appli
2	15.4	81.1	601	4	US-09-949-016-136302 Sequence 136302,
3	15.4	81.1	2338	4	US-09-582-337-1 Sequence 1, Appli
4	15.4	81.1	2350	3	US-09-187-478-1 Sequence 1, Appli
5	15.4	81.1	2350	3	US-09-292-036-1 Sequence 1, Appli
6	15.4	81.1	51049	4	US-09-949-016-15571 Sequence 15571, A
7	15	78.9	636	4	US-09-902-540-8517 Sequence 8517, Ap
8	15	78.9	6855	4	US-09-902-540-897 Sequence 897, App
9	14.8	77.9	99	2	US-08-427-097-12 Sequence 12, Appl
10	14.8	77.9	99	2	US-08-878-957-12 Sequence 12, Appl
11	14.8	77.9	170	1	US-08-419-078-5 Sequence 5, Appli
12	14.8	77.9	170	1	US-08-419-078-6 Sequence 6, Appli
13	14.8	77.9	170	1	US-08-726-883-5 Sequence 5, Appli
14	14.8	77.9	300	1	US-08-726-883-6 Sequence 6, Appli
15	14.8	77.9	300	1	US-08-419-078-4 Sequence 4, Appli
16	14.8	77.9	300	1	US-08-726-883-4 Sequence 4, Appli
17	14.8	77.9	384	4	US-09-389-681-451 Sequence 451, App
18	14.8	77.9	384	4	US-09-620-405B-451 Sequence 451, App
19	14.8	77.9	384	4	US-09-433-828B-451 Sequence 451, App
20	14.8	77.9	384	4	US-09-604-287A-451 Sequence 451, App
21	14.8	77.9	384	4	US-09-834-759-451 Sequence 451, App
22	14.8	77.9	384	4	US-09-590-751A-451 Sequence 451, App
23	14.8	77.9	384	4	US-09-551-621-451 Sequence 451, App
24	14.8	77.9	879	4	US-09-248-796A-7856 Sequence 7856, Ap
25	14.8	77.9	1322	1	US-08-419-078-1 Sequence 1, Appli
26	14.8	77.9	1322	1	US-08-726-883-1 Sequence 1, Appli
27	14.8	77.9	1323	4	US-09-023-655-55 Sequence 55, Appli

c	28	14.8	77.9	1594	4	US-09-270-767-14907	Sequence 14907, A
	29	14.8	77.9	1752	1	US-08-427-097-13	Sequence 13, Appl
	30	14.8	77.9	1752	1	US-08-427-097-19	Sequence 19, Appl
	31	14.8	77.9	1752	2	US-08-878-957-13	Sequence 13, Appl
	32	14.8	77.9	1752	2	US-08-878-957-13	Sequence 19, Appl
	33	14.8	77.9	2936	4	US-09-976-594-1044	Sequence 1044, Ap
	34	14.8	77.9	28843	4	US-09-949-016-17325	Sequence 17325, A
	35	14.8	77.9	134987	4	US-09-949-016-15348	Sequence 15348, A
	36	14.8	77.9	134987	4	US-09-949-016-15349	Sequence 15349, A
	37	14.8	77.9	134987	4	US-09-949-016-15350	Sequence 15350, A
	38	14.8	77.9	134987	4	US-09-949-016-15507	Sequence 15507, A
	39	14.8	77.9	134987	4	US-09-949-016-15508	Sequence 15508, A
	40	14.8	77.9	134987	4	US-09-949-016-15509	Sequence 15509, A
	41	14.8	77.9	203475	4	US-09-949-016-14516	Sequence 14516, A
	42	14.8	77.9	203475	4	US-09-949-016-14517	Sequence 14517, A
	43	14.8	77.9	203475	4	US-09-949-016-14518	Sequence 14518, A
	44	14.8	77.9	203475	4	US-09-949-016-14519	Sequence 14519, A
	45	14.8	77.9	203475	4	US-09-949-016-17226	Sequence 17226, A

ALIGNMENTS

RESULT 1  
US-09-552-322-1  
; Sequence 1, Application US/09552322  
; Patent No. 6436642  
; GENERAL INFORMATION:  
; APPLICANT: Gould-Rothberg  
; APPLICANT: Rastelli  
; TITLE OF INVENTION: METHOD OF CLASSIFYING A THYROID CARCINOMA USING  
; FILE REFERENCE: 15966-548  
; CURRENT APPLICATION NUMBER: US/09/552,322  
; CURRENT FILING DATE: 2000-04-19  
; PRIOR APPLICATION NUMBER: 60/130,123  
; PRIOR FILING DATE: 1999-04-20  
; PRIOR APPLICATION NUMBER: 60/193,203  
; PRIOR FILING DATE: 2000-03-30  
; NUMBER OF SEQ ID NOS: 63  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 2132  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-552-322-1

Query Match 86.3%; Score 16.4; DB 3; Length 2132;  
Best Local Similarity 94.4%; Pred. No. 78;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 AATGTCATCGTCCCGGG 19  
DB 844 AATGTCATCGTCCCGAG 861

RESULT 2  
US-09-949-016-136302  
; Sequence 136302, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 136302  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-136302

Query Match 81.1%; Score 15.4; DB 4; Length 601;  
Best Local Similarity 94.1%; Pred. No. 2.2e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 ATGTCATCGTCCCGGG 19  
||||| |||||  
Db 61 ATGTCATTGTCCTCCGGG 77

## RESULT 3

US-09-582-337-1/c  
; Sequence 1, Application US/09582337  
; Patent No. 6562618

## GENERAL INFORMATION:

; APPLICANT: Japan Tobacco, Inc.  
; TITLE OF INVENTION: Monoclonal Antibody Against Connective Tissue Growth Factor  
; FILE REFERENCE: J1-009PCT  
; CURRENT APPLICATION NUMBER: US/09/582,337  
; CURRENT FILING DATE: 2000-06-23  
; PRIOR APPLICATION NUMBER: JP P1997-367699  
; PRIOR FILING DATE: 1997-12-25  
; PRIOR APPLICATION NUMBER: JP P1998-356183  
; PRIOR FILING DATE: 1998-12-15  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 1

LENGTH: 2338

TYPE: DNA

ORGANISM: Rat

FEATURE:

NAME/KEY: 5'UTR

LOCATION: (1)..(212)

NAME/KEY: CDS

LOCATION: (213)..(1256)

NAME/KEY: 3'UTR

LOCATION: (1257)..(2338)

NAME/KEY: polyA signal

LOCATION: (2297)..(2302)

US-09-582-337-1

Query Match 81.1%; Score 15.4; DB 4; Length 2338;  
Best Local Similarity 94.1%; Pred. No. 2.5e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 ATGTCATCGTCCCGGG 19  
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Db 1210 ATGTCATTGTCCTCCGGG 1194

## RESULT 4

US-09-187-478-1/c  
; Sequence 1, Application US/09187478  
; Patent No. 6348329

## GENERAL INFORMATION:

; APPLICANT: Schmidt, Brian F.  
; APPLICANT: Allen, Margaret L.  
; TITLE OF INVENTION: Connective Tissue Growth (CTGF) And Methods Of Use  
; FILE REFERENCE: 08766/004001  
; CURRENT APPLICATION NUMBER: US/09/187,478  
; CURRENT FILING DATE: 1998-11-06  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 2350

; TYPE: DNA  
; ORGANISM: No. 6348329mal Rate Kidney Fibroblast  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (212)..(1252)  
US-09-187-478-1

Query Match 81.1%; Score 15.4; DB 3; Length 2350;  
Best Local Similarity 94.1%; Pred. No. 2.5e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 ATGTCATCGTCCCGGG 19  
||||| |||||  
Db 1209 ATGTCATTGTCCTCCGGG 1193

## RESULT 5

US-09-292-036-1/c

; Sequence 1, Application US/09292036

; Patent No. 6358741

; GENERAL INFORMATION:

; APPLICANT: FIBROGEN, INC

; APPLICANT: SCHMIDT, Brian

; APPLICANT: ALLEN, Margaret

; APPLICANT: SVERDRUP, Fran

; APPLICANT: CARMICHAEL, David

; TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR (CTGF) AND METHODS OF USE

; FILE REFERENCE: FIBRO100-1

; CURRENT APPLICATION NUMBER: US/09/292,036

; CURRENT FILING DATE: 1999-04-14

; PRIOR APPLICATION NUMBER: US 09/292,036

; PRIOR FILING DATE: 1999-04-14

; PRIOR APPLICATION NUMBER: US 09/187,478

; PRIOR FILING DATE: 1998-11-06

; NUMBER OF SEQ ID NOS: 18

; SOFTWARE: PatentIn version 3.0

SEQ ID NO 1

LENGTH: 2350

TYPE: DNA

ORGANISM: Rat

FEATURE:

NAME/KEY: CDS

LOCATION: (212)..(1252)

US-09-292-036-1

Query Match 81.1%; Score 15.4; DB 3; Length 2350;  
Best Local Similarity 94.1%; Pred. No. 2.5e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 ATGTCATCGTCCCGGG 19  
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Db 1209 ATGTCATTGTCCTCCGGG 1193

## RESULT 6

US-09-949-016-15571/c

; Sequence 15571, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 15571  
; LENGTH: 51049  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-15571

Query Match 81.1%; Score 15.4; DB 4; Length 51049;  
Best Local Similarity 94.1%; Pred. No. 3.3e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 ATGTCATCGTCCCGGG 19  
Db 13225 ATGTCATGTCCTCCCGGG 13209

## RESULT 7

US-09-902-540-8517/c  
; Sequence 8517, Application US/09902540  
; Patent No. 6833447  
; GENERAL INFORMATION:  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Wiegand, Roger C.  
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof  
; FILE REFERENCE: 38-10(15849)B  
; CURRENT APPLICATION NUMBER: US/09/902,540  
; CURRENT FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: 60/217,883  
; PRIOR FILING DATE: 2000-07-10  
; NUMBER OF SEQ ID NOS: 16825  
; SEQ ID NO 8517  
; LENGTH: 636  
; TYPE: DNA  
; ORGANISM: Myxococcus xanthus  
US-09-902-540-8517

Query Match 78.9%; Score 15; DB 4; Length 636;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GTCATCGTCCCGGG 19  
Db 279 GTCATCGTCCCGGG 265

## RESULT 8

US-09-902-540-897/c  
; Sequence 897, Application US/09902540  
; Patent No. 6833447  
; GENERAL INFORMATION:  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Wiegand, Roger C.  
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof  
; FILE REFERENCE: 38-10(15849)B  
; CURRENT APPLICATION NUMBER: US/09/902,540  
; CURRENT FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: 60/217,883  
; PRIOR FILING DATE: 2000-07-10  
; NUMBER OF SEQ ID NOS: 16825  
; SEQ ID NO 897  
; LENGTH: 6855  
; TYPE: DNA  
; ORGANISM: Myxococcus xanthus  
US-09-902-540-897

Query Match 78.9%; Score 15; DB 4; Length 6855;  
Best Local Similarity 100.0%; Pred. No. 4.4e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GTCATCGTCCCGGG 19

Db 4057 GTCATCGTCCCGGG 4043

## RESULT 9

US-08-427-097-12  
; Sequence 12, Application US/08427097  
; Patent No. 5668294  
; GENERAL INFORMATION:  
; APPLICANT: Meagher, Richard B.  
; APPLICANT: Sommers, Anne O.  
; TITLE OF INVENTION: Metal Resistance Sequences and  
; TITLE OF INVENTION: Transgenic Plants  
; NUMBER OF SEQUENCES: 30  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.  
; STREET: 5370 Manhattan Circle, Suite 201  
; CITY: Boulder  
; STATE: CO  
; COUNTRY: US  
; ZIP: 80303  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/427,097  
; FILING DATE: 21-APR-1995  
; CLASSIFICATION: 800  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ferber, Donna M.  
; REGISTRATION NUMBER: 33,878  
; REFERENCE/DOCKET NUMBER: 40-94  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (303) 499-8080  
; TELEFAX: (303) 499-8089  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 99 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
; DESCRIPTION: /desc = "Oligonucleotide"  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
US-08-427-097-12

Query Match 77.9%; Score 14.8; DB 1; Length 99;  
Best Local Similarity 88.9%; Pred. No. 3.8e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TAATGTCATCGTCCCGG 18  
Db 79 TATTGTCATCGACCCCGG 96

## RESULT 10

US-08-878-957-12  
; Sequence 12, Application US/08878957  
; Patent No. 5965796  
; GENERAL INFORMATION:  
; APPLICANT: Meagher, Richard B.  
; APPLICANT: Sommers, Anne O.  
; APPLICANT: Rugh, Clayton L.  
; TITLE OF INVENTION: Metal Resistance Sequences and  
; TITLE OF INVENTION: Transgenic Plants  
; NUMBER OF SEQUENCES: 34  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.  
; STREET: 5370 Manhattan Circle, Suite 201  
; CITY: Boulder

```
STATE: Colorado
COUNTRY: US
ZIP: 80303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/878,957
FILING DATE: 19-JUN-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/427,097
FILING DATE: 21-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Ferber, Donna M.
REGISTRATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER: 40-94A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080
TELEFAX: (303) 499-8089
TELEX:
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 99 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Oligonucleotide"
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-878-957-12

Query Match 77.9%; Score 14.8; DB 2; Length 99;
Best Local Similarity 88.9%; Pred. No. 3.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TAATGTCATCGTCCCGG 18
DB 79 TATGTCATGACCCCGG 96

RESULT 11
US-08-419-078-5/c
; Sequence 5, Application US/08419078
; Patent No. 5587306
; GENERAL INFORMATION:
; APPLICANT: HAWKINS, PHILLIP R.
; APPLICANT: SEILHAMER, JEFFREY J.
; TITLE OF INVENTION: PHOSPHOLIPASE C HOMOLOG
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3330 HILLVIEW AVENUE
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/419,078
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: LUTHER, BARBARA J.
; REGISTRATION NUMBER: 33954
; REFERENCE/DOCKET NUMBER: PF0030 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-855-0572
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 170 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; IMMEDIATE SOURCE:
; LIBRARY: Fibroblast
; CLONE: 054216
US-08-419-078-6

Query Match 77.9%; Score 14.8; DB 1; Length 170;
Best Local Similarity 88.9%; Pred. No. 4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 AATGTCATCGTCCCGG 19
DB 134 AATGTCATCTCCACGG 117

TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-855-0572
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 170 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
IMMEDIATE SOURCE:
LIBRARY: Corneal Stroma
CLONE: 046611
US-08-419-078-5

Query Match 77.9%; Score 14.8; DB 1; Length 170;
Best Local Similarity 88.9%; Pred. No. 4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 AATGTCATCGTCCCGG 19
DB 134 AATGTCATCTCCACGG 117

RESULT 12
US-08-419-078-6/c
; Sequence 6, Application US/08419078
; Patent No. 5587306
; GENERAL INFORMATION:
; APPLICANT: HAWKINS, PHILLIP R.
; APPLICANT: SEILHAMER, JEFFREY J.
; TITLE OF INVENTION: PHOSPHOLIPASE C HOMOLOG
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3330 HILLVIEW AVENUE
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/419,078
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: LUTHER, BARBARA J.
; REGISTRATION NUMBER: 33954
; REFERENCE/DOCKET NUMBER: PF0030 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-855-0572
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 170 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; IMMEDIATE SOURCE:
; LIBRARY: Fibroblast
; CLONE: 054216
US-08-419-078-6

Query Match 77.9%; Score 14.8; DB 1; Length 170;
Best Local Similarity 88.9%; Pred. No. 4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 AATGTCATCGTCCCGG 19
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Db 134 AATGTCATCTCCACGGG 117  
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RESULT 13  
US-08-726-883-5/c  
; Sequence 5, Application US/08726883  
; Patent No. 5676946  
; GENERAL INFORMATION:  
; APPLICANT: HAWKINS, PHILLIP R.  
; APPLICANT: SEILHAMER, JEFFREY J.  
; TITLE OF INVENTION: PHOSPHOLIPASE C HOMOLOG  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
; STREET: 3330 HILLVIEW AVENUE  
; CITY: PALO ALTO  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/726,883  
; FILING DATE: 04-OCT-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/419,078  
; FILING DATE: 10-APR-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: LUTHER, BARBARA J.  
; REGISTRATION NUMBER: 33954  
; REFERENCE/DOCKET NUMBER: PF0030 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-855-0555  
; TELEFAX: 415-855-0572  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 170 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; IMMEDIATE SOURCE:  
; LIBRARY: Corneal Stroma  
; CLONE: 046611  
US-08-726-883-5

Query Match 77.9%; Score 14.8; DB 1; Length 170;  
Best Local Similarity 88.9%; Pred. No. 4e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 AATGTCATCTCCACGGG 19  
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Db 134 AATGTCATCTCCACGGG 117

RESULT 14  
US-08-726-883-6/c  
; Sequence 6, Application US/08726883  
; Patent No. 5676946  
; GENERAL INFORMATION:  
; APPLICANT: HAWKINS, PHILLIP R.  
; APPLICANT: SEILHAMER, JEFFREY J.  
; TITLE OF INVENTION: PHOSPHOLIPASE C HOMOLOG  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
; STREET: 3330 HILLVIEW AVENUE  
; CITY: PALO ALTO

; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/726,883  
; FILING DATE: 04-OCT-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/419,078  
; FILING DATE: 10-APR-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: LUTHER, BARBARA J.  
; REGISTRATION NUMBER: 33954  
; REFERENCE/DOCKET NUMBER: PF0030 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-855-0555  
; TELEFAX: 415-855-0572  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 170 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; IMMEDIATE SOURCE:  
; LIBRARY: Fibroblast  
; CLONE: 054216  
US-08-726-883-6

Query Match 77.9%; Score 14.8; DB 1; Length 170;  
Best Local Similarity 88.9%; Pred. No. 4e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 AATGTCATCTCCACGGG 19  
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Db 134 AATGTCATCTCCACGGG 117

RESULT 15  
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; Sequence 4, Application US/08419078  
; Patent No. 5587306  
; GENERAL INFORMATION:  
; APPLICANT: HAWKINS, PHILLIP R.  
; APPLICANT: SEILHAMER, JEFFREY J.  
; TITLE OF INVENTION: PHOSPHOLIPASE C HOMOLOG  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
; STREET: 3330 HILLVIEW AVENUE  
; CITY: PALO ALTO  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/419,078  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: LUTHER, BARBARA J.  
; REGISTRATION NUMBER: 33954  
; REFERENCE/DOCKET NUMBER: PF0030 US  
; TELECOMMUNICATION INFORMATION:

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; TELEPHONE: 415-855-0555
; TELEFAX: 415-855-0572
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 300 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; LIBRARY: Hybrid T/B Lymphoblast
; CLONE: 043866
US-08-419-078-4

Query Match      77.9%; Score 14.8; DB 1; Length 300;
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Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db      256 AATGTCATCTCCACGGG 239
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Job time : 6.05825 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: April 12, 2005, 04:59:42 ; Search time 14.1055 Seconds  
(without alignments)  
8162.777 Million cell updates/sec

Title: US-09-979-558A-2

Perfect score: 19

Sequence: 1 taatgtcatcgtccccggg 19

Scoring table: IDENTITY\_NUC

Gapop 10\_0 , Gapext 1.0

Searched: 5615251 seqs, 3030001701 residues

Total number of hits satisfying chosen parameters: 11230502

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications\_NA:\*

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- 3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*
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- 11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq:\*
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- 15: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:\*
- 16: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq:\*
- 17: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq:\*
- 18: /cgn2\_6/ptodata/1/pubpna/US10F\_PUBCOMB.seq:\*
- 19: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq:\*
- 20: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq:\*
- 21: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*
- 22: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	16.4	86.3	1329	17	US-10-169-395-18
2	16.4	86.3	1882	9	US-09-925-298-301
3	16.4	86.3	1882	14	US-10-102-806-301
4	16.4	86.3	1926	9	US-09-764-853-238
5	16.4	86.3	1987	9	US-09-818-143-20
6	16.4	86.3	1989	10	US-09-946-374-76
7	16.4	86.3	1989	14	US-10-006-856A-76
8	16.4	86.3	1989	14	US-10-006-818A-76
9	16.4	86.3	1989	14	US-10-006-485A-76
10	16.4	86.3	1989	14	US-10-013-907A-76
11	16.4	86.3	1989	14	US-10-015-499A-76

12	16.4	86.3	1989	14	US-10-015-393A-76	Sequence 76, Appl
13	16.4	86.3	1989	14	US-10-015-869A-76	Sequence 76, Appl
14	16.4	86.3	1989	14	US-10-012-121A-76	Sequence 76, Appl
15	16.4	86.3	1989	14	US-10-006-116A-76	Sequence 76, Appl
16	16.4	86.3	1989	14	US-10-006-117A-76	Sequence 76, Appl
17	16.4	86.3	1989	14	US-10-017-527A-76	Sequence 76, Appl
18	16.4	86.3	1989	14	US-10-013-913A-76	Sequence 76, Appl
19	16.4	86.3	1989	14	US-10-007-194A-76	Sequence 76, Appl
20	16.4	86.3	1989	14	US-10-013-430A-76	Sequence 76, Appl
21	16.4	86.3	1989	14	US-10-011-671A-76	Sequence 76, Appl
22	16.4	86.3	1989	14	US-10-012-755A-76	Sequence 76, Appl
23	16.4	86.3	1989	14	US-10-015-386A-76	Sequence 76, Appl
24	16.4	86.3	1989	15	US-10-011-692A-76	Sequence 76, Appl
25	16.4	86.3	1989	15	US-10-006-768A-76	Sequence 76, Appl
26	16.4	86.3	1989	15	US-10-017-610A-76	Sequence 76, Appl
27	16.4	86.3	1989	15	US-10-006-063A-76	Sequence 76, Appl
28	16.4	86.3	1989	15	US-10-020-063A-76	Sequence 76, Appl
29	16.4	86.3	1989	15	US-10-015-391A-76	Sequence 76, Appl
30	16.4	86.3	1989	15	US-10-017-407A-76	Sequence 76, Appl
31	16.4	86.3	1989	15	US-10-011-833A-76	Sequence 76, Appl
32	16.4	86.3	1989	15	US-10-006-041A-76	Sequence 76, Appl
33	16.4	86.3	1989	15	US-10-015-822A-76	Sequence 76, Appl
34	16.4	86.3	1989	15	US-10-015-387A-76	Sequence 76, Appl
35	16.4	86.3	1989	15	US-10-006-130A-76	Sequence 76, Appl
36	16.4	86.3	1989	16	US-10-006-172A-76	Sequence 76, Appl
37	16.4	86.3	1989	16	US-10-017-253A-76	Sequence 76, Appl
38	16.4	86.3	1989	16	US-10-015-392A-76	Sequence 76, Appl
39	16.4	86.3	1989	16	US-10-017-306A-76	Sequence 76, Appl
40	16.4	86.3	1989	16	US-10-017-867A-76	Sequence 76, Appl
41	16.4	86.3	1989	16	US-10-012-064A-76	Sequence 76, Appl
42	16.4	86.3	1989	16	US-10-013-909A-76	Sequence 76, Appl
43	16.4	86.3	1989	16	US-10-015-671A-76	Sequence 76, Appl
44	16.4	86.3	1989	16	US-10-015-610A-76	Sequence 76, Appl
45	16.4	86.3	1989	16	US-10-012-137A-76	Sequence 76, Appl

ALIGNMENTS

RESULT 1  
US-10-169-395-18  
; Sequence 18, Application US/10169395  
; Publication No. US20040034192A1  
; GENERAL INFORMATION:  
; APPLICANT: KATO, Seishi  
; APPLICANT: KIMURA, Tomoko  
; TITLE OF INVENTION: HUMAN PROTEINS HAVING HYDROPHOBIC DOMAINS AND DNAS ENCODING  
; TITLE OF INVENTION: THESE PROTEINS  
; FILE REFERENCE: 01997.015100.US  
; CURRENT APPLICATION NUMBER: US/10/169,395  
; CURRENT FILING DATE: 2002-11-29  
; PRIOR APPLICATION NUMBER: JP 2000-585  
; PRIOR FILING DATE: 2000-01-06  
; PRIOR APPLICATION NUMBER: JP 2000-588  
; PRIOR FILING DATE: 2000-01-06  
; PRIOR APPLICATION NUMBER: JP 2000-2299  
; PRIOR FILING DATE: 2000-01-11  
; PRIOR APPLICATION NUMBER: JP 2000-26862  
; PRIOR FILING DATE: 2000-02-03  
; PRIOR APPLICATION NUMBER: JP 2000-58367  
; PRIOR FILING DATE: 2000-03-03  
; PRIOR APPLICATION NUMBER: PCT/JP00/09359  
; PRIOR FILING DATE: 2000-12-28  
; NUMBER OF SEQ ID NOS: 150  
; SEQ ID NO 18  
; LENGTH: 1329  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-169-395-18

Query Match 86.3%; Score 16.4; DB 17; Length 1329;  
Best Local Similarity 94.4%; Pred. No. 1.4e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;



Query Match 86.3%; Score 16.4; DB 9; Length 1987;  
Best Local Similarity 94.4%; Pred. No. 1.4e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 AATGTCATCGTCCCGGG 19  
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Db 716 AATGTCATCGTCCCGAG 733

## RESULT 6

US-09-946-374-76  
; Sequence 76, Application US/09946374  
; Publication No. US20030073129A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2830PIC1  
; CURRENT APPLICATION NUMBER: US/09/946,374  
; CURRENT FILING DATE: 2001-09-04  
; PRIOR APPLICATION NUMBER: 60/098716  
; PRIOR FILING DATE: 1998-09-01  
; PRIOR APPLICATION NUMBER: 60/098723  
; PRIOR FILING DATE: 1998-09-01  
; PRIOR APPLICATION NUMBER: 60/098749  
; PRIOR FILING DATE: 1998-09-01  
; PRIOR APPLICATION NUMBER: 60/098750  
; PRIOR FILING DATE: 1998-09-01  
; PRIOR APPLICATION NUMBER: 60/098803  
; PRIOR FILING DATE: 1998-09-02  
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; PRIOR APPLICATION NUMBER: 60/102207  
; PRIOR FILING DATE: 1998-09-29

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;; PRIOR APPLICATION NUMBER: 60/106023  
;; PRIOR FILING DATE: 1998-10-28

Query Match 86.3%; Score 16.4; DB 14; Length 1989;  
Best Local Similarity 94.4%; Pred. No. 1.4e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
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Db 715 AATGTCATCGTCCCGG 732  
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; Sequence 76, Application US/10013907A  
; Publication No. US20030064925A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan I.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2830PIC34  
; CURRENT APPLICATION NUMBER: US/10/013,907A  
; CURRENT FILING DATE: 2001-12-10  
; Prior Application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 477  
; SEQ ID NO 76  
; LENGTH: 1989  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-013-907A-76

Query Match 86.3%; Score 16.4; DB 14; Length 1989;  
Best Local Similarity 94.4%; Pred. No. 1.4e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2 AATGTCATCGTCCCGG 19

Db 715 AATGTCATCGTCCCGG 732  
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; Sequence 76, Application US/10015499A  
; Publication No. US20030065142A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan I.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2830PIC42  
; CURRENT APPLICATION NUMBER: US/10/015,499A  
; CURRENT FILING DATE: 2001-12-11  
; Prior Application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 477  
; SEQ ID NO 76  
; LENGTH: 1989



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; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-015-499A-76

Query Match      86.3%; Score 16.4; DB 14; Length 1989;
Best Local Similarity 94.4%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db      715 AATGTCATCGTCCCGAG 732

RESULT 12
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; Sequence 76, Application US/10015393A
; Publication No. US20030069179A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830PIC46
; CURRENT APPLICATION NUMBER: US/10/015,393A
; CURRENT FILING DATE: 2002-06-10
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 76
; LENGTH: 1989
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-015-393A-76

Query Match      86.3%; Score 16.4; DB 14; Length 1989;
Best Local Similarity 94.4%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 AATGTCATCGTCCCGGG 19
      |||||
Db      715 AATGTCATCGTCCCGAG 732

RESULT 13
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; Sequence 76, Application US/10015869A
; Publication No. US20030073130A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830PIC45
; CURRENT APPLICATION NUMBER: US/10/015,869A
; CURRENT FILING DATE: 2002-06-25
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 76
; LENGTH: 1989
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-015-869A-76

Query Match      86.3%; Score 16.4; DB 14; Length 1989;
Best Local Similarity 94.4%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 AATGTCATCGTCCCGGG 19
      |||||
Db      715 AATGTCATCGTCCCGAG 732

RESULT 14
US-10-012-121A-76
; Sequence 76, Application US/10012121A
; Publication No. US20030073810A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830PIC20
; CURRENT APPLICATION NUMBER: US/10/012,121A
; CURRENT FILING DATE: 2001-12-07
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 76
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-012-121A-76

Query Match      86.3%; Score 16.4; DB 14; Length 1989;
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Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db      715 AATGTCATCGTCCCGAG 732

RESULT 15
US-10-006-116A-76
; Sequence 76, Application US/10006116A
; Publication No. US20030082626A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
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Wed Apr 13 09:01:09 2005

us-09-979-558a-2.rnpb

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; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830P1C15
; CURRENT FILING DATE: 2001-12-16
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
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; PRIOR APPLICATION NUMBER: 60/103314
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;	PRIOR FILING DATE:	1998-10-27
;	PRIOR APPLICATION NUMBER:	60/105881
;	PRIOR FILING DATE:	1998-10-27
;	PRIOR APPLICATION NUMBER:	60/105882
;	PRIOR FILING DATE:	1998-10-27
;	PRIOR APPLICATION NUMBER:	60/106023
;	PRIOR FILING DATE:	1998-10-28

Query Match	86.3%	Score 16.4;	DB 14;	Length 1989;
Best Local Similarity	94.4%	Pred. NO. 1.4e+02;		
Matches 17; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;

QY 2 AATGTCATCGTCCCCGGG 19  
|||  
Db 715 AATGTCATCGTCCCCGAG 732

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Job time : 17.1055 secs

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OM nucleic - nucleic search, using sw model

Run on: April 11, 2005, 19:46:51 ; Search time 325.942 Seconds  
(without alignments)  
7660.750 Million cell updates/sec

Title: US-09-979-558A-1  
Perfect score: 1526  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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4	1098.6	72.0	1501	4	US-09-821-016-5
5	1098.6	72.0	1501	4	US-09-745-476-1
6	1098.6	72.0	1501	4	US-09-748-205-1
7	1098.6	72.0	1501	4	US-09-951-720-1
8	1098.6	72.0	1501	4	US-10-411-319-1
9	1098.6	72.0	1501	4	US-10-105-305-1
10	1098.6	72.0	1501	4	US-10-266-787-5
11	1076	70.5	1467	1	US-08-114-695A-1
12	1070.8	70.2	1467	4	US-09-726-774-3
13	1069.2	70.1	1542	2	US-08-757-653-158
14	1069.2	70.1	1542	3	US-09-465-355-2
15	1069.2	70.1	1542	3	US-08-520-946-158
16	1069.2	70.1	1542	4	US-09-655-378A-158
17	1069.2	70.1	1542	4	US-09-548-998E-33
18	1062.6	69.6	1541	4	US-09-726-774-2
19	1058.2	69.3	1549	4	US-09-492-709A-89
20	1058.2	69.3	1549	4	US-09-492-709A-242
21	1058.2	69.3	1549	4	US-09-492-709A-402
22	1053.6	69.0	1518	1	US-08-114-695A-6
23	1052.4	69.0	1487	4	US-09-726-774-14
24	1039.2	68.1	1506	4	US-10-278-942-1
25	1031.2	67.6	1500	4	US-09-726-774-4
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29 1016.4 66.6 1429 4 US-09-934-868-81 Sequence 81, Appli  
30 1014.8 66.5 640681 4 US-09-790-988-1 Sequence 1, Appli  
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38 961.8 63.0 1487 4 US-09-726-774-13 Sequence 13, Appli  
39 932.8 61.1 1474 1 US-08-114-695A-8 Sequence 8, Appli  
40 931.8 61.1 1536 2 US-08-643-229A-1 Sequence 1, Appli  
41 927.8 60.8 1536 1 US-08-114-695A-7 Sequence 7, Appli  
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## ALIGNMENTS

## RESULT 1

US-09-596-002-41/c  
; Sequence 41, Application US/09596002  
; Patent No. 6632636  
; GENERAL INFORMATION:  
; APPLICANT: Legace, Robert, E.  
; APPLICANT: Patterson, Chandra  
; APPLICANT: Berg, Kim, L.  
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF MORAXELLA CATARRHALIS GENOME  
; FILE REFERENCE: PM-0008-4 US  
; CURRENT APPLICATION NUMBER: US/09/596,002  
; CURRENT FILING DATE: 2000-06-16  
; PRIOR APPLICATION NUMBER: 60/140,121  
; PRIOR FILING DATE: 1999-06-18  
; NUMBER OF SEQ ID NOS: 41  
; SOFTWARE: PERL Program  
; SEQ ID NO 41  
; LENGTH: 269223  
; TYPE: DNA  
; ORGANISM: Moraxella catarrhalis  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte template ID No. 6632636 41  
; PUBLICATION INFORMATION:  
US-09-596-002-41

Query Match 79.4%; Score 1211; DB 4; Length 269223;  
Best Local Similarity 90.6%; Pred. No. 0;  
Matches 1361; Conservative 0; Mismatches 127; Indels 15; Gaps 6;  
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Db 92724 CGATCTGTAGCTGCTCTGAGAGGATGATCACCACCTGAGGACTGAGACACGGCCCGAC 92665

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QY 504 GTGCAGCAGCGCGGTAAATACAGAGGTCGAAGCGTTAAATCGGAATTAATCTGGCGTAAA 563  
Db |||||  
QY 92484 GTGCAGCAGCGCGGTAAATACAGAGGTCGAAGCGTTAAATCGGAATTAATCTGGCGTAAA 92425  
Db |||||  
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RESULT 2  
US-08-299-810A-27  
; Sequence 27, Application US/08299810A  
; Patent No. 5721097  
; GENERAL INFORMATION:  
; APPLICANT: Rousseau, Rudi  
; APPLICANT: Van Heuverswyn, Hugo  
; TITLE OF INVENTION: HYBRIDIZATION PROBES FOR THE  
; TITLE OF INVENTION: DETECTION OF BRANHAMELLA CATARRHALIS STRAINS  
; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Merchant & Gould  
; STREET: 3100 No. 5721097west Center  
; CITY: Minneapolis  
; STATE: MN  
; COUNTRY: USA  
; ZIP: 55402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/299,810A  
; FILING DATE: 01-SEP-1994  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hillson, Randall A.  
; REGISTRATION NUMBER: 31,838  
; REFERENCE/DOCKET NUMBER: 8076.70-US-WO  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 612-332-5300  
; TELEFAX: 612-332-9081  
; INFORMATION FOR SEQ ID NO: 27:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1485 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; ORIGINAL SOURCE:  
; ORGANISM: Branhamella catarrhalis  
; IMMEDIATE SOURCE:  
; CLONE: 16S rRNA Gene  
; US-08-299-810A-27  
Query Match 78.3%; Score 1195; DB 1; Length 1485;  
Best Local Similarity 90.6%; Pred. No. 0;  
Matches 1352; Conservative 0; Mismatches 128; Indels 12; Gaps 7;  
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DB	233	GTAGCTGTCTGTAGAGGATGATCAGCCACACTGGGACTGAGACACGGCCGACACTCCCTAC	292
QY	335	GGGAGCGACGATGGGGAAATTTGGAACAATGGNGGGAACCTTGATCCAGCCATGCGCGGT	394
DB	293	GGGAGCGACGATGGGGAAATTTGGACAATGGCGAAAGCCTGATCCAGCCATGCGCGGT	352
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DB	353	GTGTGAAGAAGCCCTTTTGGTTGTAAAGCACTTTTAAGTGGGGAGGAAAAGCTTATGGTTA	412
QY	455	ATACCCGGGGACGATGACATTAGCTTGCAAGTAATAGCACCGGCTTAACCTCTGTGCCAGCAGC	514
DB	413	ATACCCATAAGCCCTGACGTTACCCACAGAATAGCACCGGCTTAACCTCTGTGCCAGCAGC	472
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DB	473	CGCGTAAATACAGAGGTGCAAGCGTTAATCGG-ATTACTGGGCGTAAAGCGCGCGTAGG	531
QY	575	TGGCTTGATAGTCAGATGTGNAATCCCGGGCTTAACTCGGAACTGCATCTGNAACTG	634
DB	532	TGGTTATTTAAAGTCAGATGTGAAGCCCGGGCTTAACTCGGAACTGCATCTGATACGT	591
QY	635	TTAGGCTAGAGTGTAGGTGAGAGGGAAGTAGAATTTTCAGGTGTAGCGGTGAAATGCGTAGAG	694
DB	592	GATAACTAGATAGGTGAGAGGGGNGTAGAATTCAGGTGTAGCGGTGAAATGCGTAGAG	651
QY	695	ATCTGAAGGAATACCGATGGCGAAGGCACTTCTTCGGCATCATACTGACACTGAGGCTCG	754
DB	652	ATCTGAGGAATACCGATGGCGAAGGCACTCCCTGGCATCATACTGACACTGAGGTCG	711
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DB	712	AAAGCTGGGTAGCAACAGAGATTAGATACCTCGTGTAGTCACCGCGTAAACGATGTCTA	771
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DB	832	GGGAGTACGGCCGCAAGGTTAAAACCTCAAATGAAATTGACGGGGGCCGCAACAAGCGGTG	891
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DB	892	AGCATGTGTTTAATTCGATCGAACGCAAGAACCTTACCTGTGTCTTGACATAGTGAGAA	951
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QY	1055	CAGCTCGTGTGATGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCTTGTCTCTTAGT	1114
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QY	1115	TACCAGCACTTCGGGTGGGAACCTTAAGGATCTGCCAGTCACAAACTGGAGGAAGCGG	1174
DB	1072	TACCAGCACTTCGGTGGGAACTCTAAGGATCTGCCAGTCACAAACTGGAGGAAGCGG	1131
QY	1175	GGACGAGCTCAAGTCATCATGGCCCTTACGACCCAGGGCTACACAGCTGCTACATGGTAG	1234
DB	1132	GGACGAGCTCAAGTCATCATGGCCCTTACGACCCAGGGCTACACAGCTGCTACATGGTAG	1191
QY	1235	GTAACAGGGCAGCTACACAGGATGTGATCGGAATCTCAAAAAGCCTATCGTAGTCAG	1294
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### RESULT 3

US-09-793-920A-1

US-03-733-920A-1  
: Sequence 1. Application US/09793920A

; Sequence 1, Application  
; Patent No. 6479621; FACEIL NO. 8475621  
; GENERAL INFORMATION:

GENERAL INFORMATION:  
APPLICANT: Canon Inc.

; APPLICANT: CANON INC.  
 ;  
 ; TITLE OF INVENTION: Polyhydroxyalkanoate containing 3-hydroxythienylalkanoic acid as  
 ;  
 ; TITLE OF INVENTION: monomer unit, and method for producing the same.  
 ;  
 ; TITLE OF INVENTION: monomer unit, and method for producing the same.

FILE OF INVENTION: 4396021  
FILE REFERENCE: 4396021

FILE REFERENCE: 4396021  
CURRENT APPLICATION NUMBER: US/09/793.920A

; CURRENT APPLICATION NUMBER: US/0  
 ; CURRENT FILING DATE: 2001-02-28

: CURRENT FILING DATE: 2  
 : NUMBER OF SEO ID NOS: 1

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; NUMBER OF SEQ
; SEQ ID NO 1

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; SEQ ID NO 1
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: LENGTH: 1501

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LENGTH: 1501  
TYPE: DNA

TYPE: DNA  
ORGANISM: *Pseudomonas jessenii* 161 strain

; ORGANISM: PS  
IIS-09-793-920A-1

Query Match	Score 1098.6;	DB 4;	Length 1501;
72.0%			

Query match	72.0%;	Score	1938.0
Best Local Similarity	85.9%;	Pred. No. 0;	

Best local similarity 83.3%; Fied. NO. 0;  
Matches 1287; Conservative 0; Mismatches 202; Indels 9; Gaps 6;

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QY 30 GGGGCAAGGCTATACACATGCAAGTCCAGCCGAAACGATAGCTTGCATATAGGGCTC 69

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209 CGCTATTAGATGAGCCTAAGTCGGATTAGCTAGATGGTGGGTAAGGCCTACCATGGCG 268

Db 184 CGCTATCAGATGAGCCTAGGTCGGATTAGCTAGTTGGTGAGGTAATGGCTACCAAGCG 243

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Db 304 CTCCTACGGGAGGCAGCAGTGGGGAATATTGGACAATGGCGGAAAGCCTGATCCAGCCAT 363

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364 CCGCGCTGTCGACGACCGCTTCCGATTCTCTACACCACTTTCCGACGACCGCAT 423

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Db 484 CAGCAGCCGGTAAATACAGAGGGTGCAGCGTTAATCGGAATTACTGGGCGTAAAGCGC 543  
Qy 568 GCGTAGTGGTGTGATAAGTGCAGATGTGAAATCCCGGGCTTAACTCTGGGAACATGCATCT 627  
Db 544 GCGTAGTGGTGTGATAAGTGTGAAAGCCCGGGCTCAACTGGGAACATGCATTC 603  
Qy 628 GAACTGTTAGCTAGTGTAGAGAGGGAAGTAGAATTTTCAGTGTAGCGGTGAATG 687  
Db 604 AAACTGACAGCTAGATGTAGAGGGTGGTGAATTTCTGTGTAGCGGTGAATG 663  
Qy 688 CGTAGATCTGAAGGAATACCGATGGCGAAGGAGCTTCTCGGCATCATACTGACACTG 747  
Db 664 CGTAGATATAGAGGAACACAGTGGCGAAGGCGACCACTGACTGATACTGACACTG 723  
Qy 748 AGGCTCGAAAGCGTGGGTAGCAACAGAGATTAGATACCTCTGGTAGTCCACCGGTAAACG 807  
Db 724 AGGTGCGAAAGCGTGGGAGCAAAAGGATTAGATACCTCTGGTAGTCCACCGGTAAACG 783  
Qy 808 ATGTCTACTAGTCTGGTCCCTTGAGGACTTGTAGCGAGCTTAAGCGCAATTAAGTAGA 867  
Db 784 ATGTCAACTACCGTGGAGCCCTTGAAGCTCTTGTAGTGGCGAGCTTAAGCGCAATTAAGTAGA 843  
Qy 868 CCGCTCGGGAGTACGGCCGCAAGGTTAAAACTCAAAATGAATTCGACGGGCGCCGCAAA 927  
Db 844 CCGCTCGGGAGTACGGCCGCAAGGTTAAAACTCAAAATGAATTCGACGGGCGCCGCAAA 903  
Qy 928 GCGGTGAGCATGTGTTTAATTCATGCAACGCGAAGAACCTTACCTGTGTACACCGGTAAACG 987  
Db 904 GCGGTGAGCATGTGTTTAATTCGAAACAAACGCGAAGAACCTTACCGAGGCTTGAATC 963  
Qy 988 CACAGAACTCTTGTAGAGATACGAGTGCCTTCCGGGAATTTGTATACAGGTGCTGCATGG 1047  
Db 964 CAATGAATCTTCCAGAGATGATGGTGCCTTCCGGGAACATTGAGACAGTGTGCAATGG 1023  
Qy 1048 CTGTCTGACGCTCGTGTGAGATGTGGGTAAAGTCCCGCAACGAGCGCAACCTTGT 1107  
Db 1024 CTGTCTGACGCTCGTGTGAGATGTGGGTAAAGTCCCGCAACGAGCGCAACCTTGT 1083  
Qy 1108 CCTAGTTACAGCAC-TTCGGGTGGNACTTAAGNTACTGCAAGTGTGCAAGTCAAACTGGAG 1166  
Db 1084 CCTAGTTACAGCACGTAATGGTGGGCACTCTAAGGAGACTGCGCGGTGCAAAACCGGAG 1143  
Qy 1167 GAAGCGGGGACGACGTCAGTCAATGCGCCCTTACGACAGGGCTACACAGTGTCTAC 1226  
Db 1144 GAAGTGGGATGACGTCAGTCAATGCGCCCTTACGGCTGGGCTACACAGTGTCTAC 1203  
Qy 1227 AATGGTAGTACAGAGGAGCTACAGAGCATGTGATGCGAATCTCAAAAGCCTATCG 1286  
Db 1204 AATGGTCGGTACAGAGGGTTGCCAAGCGCGAGGTGGAGCTTAATCCCAACAAACCGATCG 1263  
Qy 1287 TAGTCCAGATTGGAGTCTGCAACTCGACTCCATCAAGTAGGAATCGGTAGTAATCGCGGA 1346  
Db 1264 TAGTCCGATCGCAGTCTGCAACTCGACTGCGTGAAGTTCGGAATCGGTAGTAATCGCGGA 1323  
Qy 1347 TCAGAAATCGCGGTGAATAGCTTCCCGGGCTTGTACACACCGCCGCTCACACCATGGG 1406  
Db 1324 TCAGAAATCGCGGTGAATAGCTTCCCGGGCTTGTACACACCGCCGCTCACACCATGGG 1383  
Qy 1407 AGTTGATTGACACAGAGTGTGAGCTTAA-CTTAGTAGAGGCGCATCACACGCTGTGGT 1465  
Db 1384 AGTGGGTGACACAGAGTAGTCTAGTCTAACTTTCGGGAGGACGTTTACCACGCTGTGAT 1443  
Qy 1466 CGATGACTGGGGTGAAGTCGTAAACAGTAGCCGTAGCGGAACTCGGGCTGGATCAC 1523  
Db 1444 TCATGACTGGGGTGAAGTCGTAAACAGTAGCCGTAGGGNAACCTCGGGCTGGATCAC 1501

## RESULT 4

US-09-821-016-5  
; Sequence 5, Application US/09821016  
; Patent No. 6485951  
; GENERAL INFORMATION:  
; APPLICANT: CANON INC.

; TITLE OF INVENTION: Polyhydroxyalkanoate Synthase and Gene Encoding the Same Enzyme  
; FILE REFERENCE: 4051021  
; CURRENT APPLICATION NUMBER: US/09/821.016  
; CURRENT FILING DATE: 2001-03-30  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: Microsoft Word  
; SEQ ID NO. 5  
; LENGTH: 1501  
; TYPE: DNA  
; ORGANISM: Pseudomonas jessenii P161; BP-7376  
; FEATURE:  
US-09-821-016-5

## Query Match

Best Local Similarity 72.0%; Score 1098.6; DB 4; Length 1501;

Matches 1287; Conservative 0; Mismatches 202; Indels 9; Gaps 6;

Qy 30 GCGCGCAGGCTTAACACATCGAATCGAGCGGAACCATGATAGCTTGTCTATTAGGCGTC 89  
Db 9 GCGCGCAGGCTTAACACATCGAATCGAGCGG--ATGACGGGAGCTTGTCTCTGAATTCA 66  
Qy 90 GAGCNGCCGACGCGGTGAGTAATCTTATAGGAATCTACTAGTAGTGGGGGATAGCTCGGG 149  
Db 67 G---CGCGGACGCGGTGAGTAATCTGCTAGGAATCTGCTGTAGTGGGACACAGCTC 123  
Qy 150 GAAACTCGAATTAATACCGCATACGT-CTAGCGGAGAAACGAGGGGNTCAATTAGACCTTG 208  
Db 124 GAAAGGAGCCTAATACCGCATACGCTCTACGGGAGAAAGCAGGGGACCTTCGGGGCCTTG 183  
Qy 209 CGCTATTAGATGAGCCCTAAGTCGATAGTGTGGGTAAAGCCCTACCATGGCG 268  
Db 184 CGCTATCAGATGAGCCCTAGTTCGATTTAGTGTGAGGTAATGGCTCACCAAGCGG 243  
Qy 269 ACGATCTGTAGTGTCTGAGAGATGATCAGCCACACCGGGACTGAGACACGCGCCCGGA 328  
Db 244 ACGATCTGTAACTGGTCTGAGAGATGATCAGTCACACTGGAACCTGAGACACGCGTCAGA 303  
Qy 329 CT-CTAGCGGAGCAGCAGTGGGGAATATTGGCAATATTGGNGNAACCTCTGACAGCCAT 387  
Db 304 CTCTACGGGAGGAGCAGTGGGGAATATTGGCAATATTGGGCAAGGCTGATCAGGCCAT 363  
Qy 388 GCGCGCTGTGTAAGAGGCGCTTTTGGTTGTAAGCACATTTAAAGCAGTGAAGAAGACTCT 447  
Db 364 GCGCGTGTGTGAAGAAGTCTTCGGATTGTAAAGCACATTTAAGTTGGGAGGAAGGCGAT 423  
Qy 448 TCGGTTAATACCCGCGGACGATGACATTAGCTGCGAATAAGCACCGGCTAACTCTGTGC 507  
Db 424 TAACTTAATACGTTAGTGTGTTTACGCTTACCGACAGAAATAGCACCGGCTAACTCTGTGC 483  
Qy 508 CAGCAGCGCGGTAAATACAGAGGTCAGCGTTAATCGGAATTTACTGGCGGTAAAGCGGA 567  
Db 484 CAGCAGCGCGGTAAATACAGAGGTCAGCGTTAATCGGAATTTACTGGCGGTAAAGCGG 543  
Qy 568 GCGTAGTGGCTTTGATAAGTTCAGATGTGAATCCCGGGCTTAACTCTGGGAACATGCACT 627  
Db 544 GCGTAGTGGCTTTGTTAAGTTGATGTGAAGCCCCCGGGCTCAACTCTGGGAATGCACTTC 603  
Qy 628 GAACTGTTAGCTAGATGTAGAGGGAAGTAGAATTTTCAGTGTAGCGGTGAATG 687  
Db 604 AAACTGACAAAGCTAGAGTATGTTAGAGGGTGGTGAATTTCTGTGTAGCGGTGAATG 663  
Qy 688 CGTAGAGATCTGAAGGAATACCGATGGCGAAGGCGAGCTTCTCTGGCATCATACTGACACTG 747  
Db 664 CGTAGATATAGGAAGGAACACCACTAGTGGGAGGCGACCACTGACTGATACTGACACTG 723  
Qy 748 AGGCTCGAAAGCGTGGGTAGCAAAAGGATTAGATACCTCTGGTAGTCCACCGGTAAACG 807  
Db 724 AGGTGCGAAAGCGTGGGAGCAAAAGGATTAGATACCTCTGGTAGTCCACCGGTAAACG 783  
Qy 808 ATGTCTACTAGTGTGGGTCCCTCTGAGGACTTGTAGTACGACAGTAAACGCAATTAAGTAGA 867  
Db 784 ATGTCAACTAGCCCTTGGGAGCCCTTGAAGCTCTTGTAGTGGCGCACTAACGCAATTAAGTTGA 843



QY 868 CCGCTGGGAGTACGGCGCAAGGTTAAATCTCAAAATGAATGACGGGGGCCGACAA 927  
| | | | |  
Db 844 CCGCTGGGAGTACGGCGCAAGGTTAAATCTCAAAATGAATGACGGGGGCCGACAA 903  
| | | | |  
QY 928 CCGGTGGAGCATGTGGTTAAATTCATGCAACGCGAAGAACCTTACCTGGTCTTGACATA 987  
| | | | |  
Db 904 CCGGTGGAGCATGTGGTTAAATTCGAAGCAACGCGAAGAACCTTACCGAGGCTTGACATC 963  
| | | | |  
QY 988 CACAAATCTTTGATAGATACGAGAGTGCCTTCGGGAATTTGATACAGGTGCTGCATGG 1047  
| | | | |  
Db 964 CAATGAATCTTCAGAGATGAGTGGTCTTCGGGAACATTTGAGACAGGTGCTGCATGG 1023  
| | | | |  
QY 1048 CTGTCGTGAGTCTGCTGAGATGTTGGGTAAAGTCCCGCAACGAGCGCAACCTTTGT 1107  
| | | | |  
Db 1024 CTGTCGTGAGTCTGCTGAGATGTTGGGTAAAGTCCCGTAACGAGCGCAACCTTTGT 1083  
| | | | |  
QY 1108 CCTAGTTACAGCAC-TTCGGGTGGGAACCTTAAGGATACCTGCGAGTGACAACTGGAG 1166  
| | | | |  
Db 1084 CCTAGTTACAGCACGTAATGGTGGGCACTTAAGGAGACTGCCGGTGACAAACCGGAG 1143  
| | | | |  
QY 1167 GAAGCGGGGACGACGCTCAAGTCAATGCGCCCTTACGACGAGGCTACACAGCTGTAC 1226  
| | | | |  
Db 1144 GAAGTGGGATGACGCTCAAGTCAATGCGCCCTTACGGCTGGGCTACACAGCTGTAC 1203  
| | | | |  
QY 1227 AATGTAAGTACAGAGGCGAGCTACACAGCGATGTGATCGGAATCTCAAAAGCCCTATCG 1286  
| | | | |  
Db 1204 AATGTCGTTACAGAGGTTGCCAAGCGCGAGGTGGAGCTAATCCACAAACCGATCG 1263  
| | | | |  
QY 1287 TAGTCCAGATGGAGTCTGCAACTCGACTCATGAGTAGTAAGTACGCTAGTAATCGCGGA 1346  
| | | | |  
Db 1264 TAGTCCGATCGAGTCTGCAACTCGACTCGCTGTAAGTCCGAATCGCTAGTAATCGCGAA 1323  
| | | | |  
QY 1347 TCAGAAATCCCGGCTGAATACGTTCCCGGCTTGTACACACCGCGCTACACCATGG 1406  
| | | | |  
Db 1324 TCAGAAATCCCGGCTGAATACGTTCCCGGCTTGTACACACCGCGCTACACCATGG 1383  
| | | | |  
QY 1407 AGTTGATTCACAGAACTGTTAGCTAA-CTTAGTAGGCGGATACACCGGTGGT 1465  
| | | | |  
Db 1384 AGTGGTTGACCAAGAGTAGTCTAACTTCGGGAGGAGCGTTACCAAGCTGTGAT 1443  
| | | | |  
QY 1466 CGATGACTGGGGTGAAGTCGTAACAGGTAGCGGTAGGGAACCTTGGGCTGGATCAC 1523  
| | | | |  
Db 1444 TCATGACTGGGGTGAAGTCGTAACAGGTAGCGGTAGGGAACCTTGGGCTGGATCAC 1501  
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## RESULT 5

US-09-745-476-1

; Sequence 1, Application US/09745476

; Patent No. 6521429

; GENERAL INFORMATION:

; APPLICANT: CANON INC.

; TITLE OF INVENTION: Preparation of Poly-hydroxyalkanoic Acid

; FILE REFERENCE: 4351008

; CURRENT APPLICATION NUMBER: US/09/745,476

; CURRENT FILING DATE: 2000-12-26

; NUMBER OF SEQ ID NOS: 1

; SOFTWARE: Microsoft Word

; SEQ ID NO 1

; LENGTH: 1501

; TYPE: DNA

; ORGANISM: Pseudomonas jessenii P161 ; FERM P-17445

US-09-745-476-1

Query Match 72.0%; Score 1098.6; DB 4; Length 1501;

Best Local Similarity 85.9%; Pred. No. 0;

Matches 1287; Conservative 0; Mismatches 202; Indels 9; Gaps 6;

QY 30 GCGCGGAGCTTAACATGCAAGTCGAGCGGAACAGATAGCTTCTGCTATTAGCGTC 89

| | | | |

Db 9 GCGCGGAGCTTAACATGCAAGTCGAGCGG--ATGACGGGAGCTTCTCTGAATTCA 66

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QY 90 GAGNCGCGGACGGGTGAGTAATCTTAGGAATCTTACCTAGTAGTGGGGGATAGCTCGG 149

| | | | |

Db 67 G---CGGCGGACGGGTGAGTAATCTAGGAATCTGCTGCTAGTGGGGGACAACTCTC 123  
| | | | |  
QY 150 GAACTCCAAATTAATACCGCATACGT-CTACGGGAGAAAGCAGGGGNTCATTTAGACCTTGT 208  
| | | | |  
Db 124 GAAAGGAGCGCTTAATACCGCATACGTCTTAACGGGAGAAAGCAGGGGACCTTCGGGGCTTGT 183  
| | | | |  
QY 209 CGCTATTAGATGAGCCTTAAGTCGATTAAGTGGTGGGTAAAGGCTTACCAATGGCG 268  
| | | | |  
Db 184 CGCTATCAGATGAGCCTTAGCTCGGATTAGTGGTGGTAAAGGCTTACCAATGGCG 243  
| | | | |  
QY 269 ACGATCTGTAGCTGTCTGAGAGGATGATACGCCACACCGGAGCTGAGACACGGCCGGA 328  
| | | | |  
Db 244 ACGATCCGTAATCTGTCTGAGAGGATGATCAGTCACTGGAACTGAGACACGGTCCAGA 303  
| | | | |  
QY 329 CT-CTACGGGAGGAGCAGCTGGGGAATATTGGCAATCGGNGGAACTCTGATCCAGCCAT 387  
| | | | |  
Db 304 CTCTTACCGGAGGAGCAGCTGGGGAATATTGGCAATCGGNGGAACTCTGATCCAGCCAT 363  
| | | | |  
QY 388 GCCGCGTGTGTGAAGAAGCCCTTTTGGTGTGTAAAGCACTTTAAAGCAGTGAAGAAGACTCT 447  
| | | | |  
Db 364 GCCGCGTGTGTGAAGAAGCTCTTCGGAATGTAAAGCACTTTAAAGTGGGAGGAAGGCAT 423  
| | | | |  
QY 448 TCGGTTAATACCCGGGAGCAGATGACATTAGCTGCGAATAAGACACCGGCTAACTCTGTGC 507  
| | | | |  
Db 424 TAACTTAATACGTTAGTGTGTTTACGTTACCGACAGAAATAAGCACCGGCTAACTCTGTGC 483  
| | | | |  
QY 508 CAGCAGCGCGGTAATACAGAGGGTGCAGGCTTAATCGGAATTACTGGGCGTAAAGCGA 567  
| | | | |  
Db 484 CAGCAGCGCGGTAATACAGAGGGTGCAGGCTTAATCGGAATTACTGGGCGTAAAGCGC 543  
| | | | |  
QY 568 CGGTAGTGGCTTGATTAAGTCAGATGTGAATATCCCGGGCTTAACTGGGAACTGCATCT 627  
| | | | |  
Db 544 CGGTAGTGGCTTGTTAAGTTGGATGTGAAGCCCCGGGCTCAACTGGGAACTGCATTC 603  
| | | | |  
QY 628 GAACTGTAGGCTAGAGTAGGTGAGAGGAAGTAGAATTTTCAGGTGTAGCGGTGAAATG 687  
| | | | |  
Db 604 AAAATCTCAAGCTAGAGTATGTTAGAGGGTGTGGAAATTTCTCTGTAGCGGTGAAATG 663  
| | | | |  
QY 688 CGTAGATCTGAAGGAATACCGATGGCGAAGGAGCTTCTTGGCATCATCTACACACTG 747  
| | | | |  
Db 664 CGTAGATATGAAGGAAGAACACAGTGGCGAAGGCGAACCTTGGACTGATCTACACTG 723  
| | | | |  
QY 748 AGGCTCGAAACGCTGGGTAGCAAAACAGGATTAGATACCTCTGGTAGTCCACGCGTAAACG 807  
| | | | |  
Db 724 AGGTGCGAAACGCTGGGAGCAACAGGATTAGATACCTCTGGTAGTCCACGCGTAAACG 783  
| | | | |  
QY 808 ATGTCTACTAGTCTGTGGTCCCTTTAGGAATTAGTGAACGAGCTTAACGCAATAAGTAGA 867  
| | | | |  
Db 784 ATGTCAACTAGCCGTTGGGAGCTTTGAGCTCTTAGTGGCGCAGCTTAACGCAATAAGTTGA 843  
| | | | |  
QY 868 CCGCTTGGGAGTACGGCCGCAAGGTTAAACTCAAAATGAATTCAGCGGGGCCGACAA 927  
| | | | |  
Db 844 CCGCTTGGGAGTACGGCCGCAAGGTTAAACTCAAAATGAATTCAGCGGGGCCGACAA 903  
| | | | |  
QY 928 CCGGTGGAGCATGTGGTTAATTCGATGCAACGCGAAGAACTTACCTTGGTCTTGACATA 987  
| | | | |  
Db 904 CCGGTGGAGCATGTGGTTAATTCGAGCAACGCGAAGAACTTACCAAGGCTTGGACATC 963  
| | | | |  
QY 988 CACAGAAATCTTTGATAGATACGAGAGTGCCTTTCGGGAATTTGTGATACAGGTGCTGCATGG 1047  
| | | | |  
Db 964 CAATGAATCTTTCCAGAGATGAGTGGTGGCTTTCGGGAACATTTGAGACAGGTGCTGCATGG 1023  
| | | | |  
QY 1048 CTGTGCTGAGCTCGTGTGAGATGTTGGGTAAAGTCCCGCAACGAGCGCAACCTTGT 1107  
| | | | |  
Db 1024 CTGTGCTGAGCTCGTGTGAGATGTTGGGTAAAGTCCCGTAACGAGCGCAACCTTGT 1083  
| | | | |  
QY 1108 CTTTAGTTACAGCAC-TTCGGGTGGGAACCTTCAAGGATACCTGCGAGTGACAAACTGGAG 1166  
| | | | |  
Db 1084 CTTTAGTTACAGCACCGTAATGGTGGCACTCTTAAGGAGACTGCGGTGACAAACCGGAG 1143  
| | | | |  
QY 1167 GAAGCGGGGACGAGCTCAAGTCAATGAGCCCTTTACGACAGGCTTACACAGCTGTAC 1226  
| | | | |  
Db 1144 GAAGTGGGATGAGCTCAAGTCAATGAGCCCTTTACGGCTGGGCTACACAGCTGTAC 1203  
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QY 1227 AATGGTAGGTACAGAGGCGAGCTACACAGCGATGTGATCGAATCTCAAAAGCCTATCG 1286  
Db 1204 AATGGTCGTACAGAGGGTTCCCAAGCGCGAGTGGAGCTTAATCCACAAAACCGATCG 1263  
QY 1287 TAGTCCAGATTGGAGTCTGCAACTCGACTCATGAAGTAGGAATCGGTAGTAATCGCGGA 1346  
Db 1264 TAGTCCGAGTCGAGTCTGCAACTCGACTCGGTGAGTTCGGAATCGGTAGTAATCGCGAA 1323  
QY 1347 TCAGAAATGCCCGGTGAATAGCTTCCCGGGCTTTGTACACACCCCGCTCACACCATGGG 1406  
Db 1324 TCAGAAATGTCGGGTGAATAGCTTCCCGGGCTTTGTACACACCCCGCTCACACCATGGG 1383  
QY 1407 AGTTGATTGACACAGAGTGTGTAGCTAA-CTTAGTAGAGGCGCATCACACGTTGGT 1465  
Db 1384 AGTGGGTGACACAGAGTGTGTAGCTAACTTTCGGGAGGACGGTTACACCGTGTGAT 1443  
QY 1466 CGATGACTGGGGTCAAGTCTGTAACAAGTAGCCGTAGGGAACTTCGGCTTGGATCAC 1523  
Db 1444 TCATGACTGGGGTGAAGTCTGTAACAAGTAGCCGTAGGGAACTTCGGCTTGGATCAC 1501

RESULT 6  
US-09-748-205-1  
; Sequence 1, Application US/09748205  
; Patent No. 6586562  
; GENERAL INFORMATION:  
; APPLICANT: Canon Inc.  
; TITLE OF INVENTION: Polyhydroxyalkanoate its manufacturing method, and microorganism  
; TITLE OF INVENTION: those are used for the method.  
; FILE REFERENCE: 4351009  
; CURRENT APPLICATION NUMBER: US/09/748,205  
; CURRENT FILING DATE: 2000-12-27  
; NUMBER OF SEQ ID NOS: 1  
; SEQ ID NO 1  
; LENGTH: 1501  
; TYPE: DNA  
; ORGANISM: Pseudomonas jessenii 161 strain.  
US-09-748-205-1

Query Match 72.0%; Score 1098.6; DB 4; Length 1501;  
Best Local Similarity 85.9%; Pred. No. 0;  
Matches 1287; Conservative 0; Mismatches 202; Indels 9; Gaps 6;  
QY 30 GCGCGAGGCTTACACATCGCAAGTCTGAGCGGAACGATAGCTTGTCTATTAGGCGTC 89  
Db 9 GCGCGAGGCTTACACATCGCAAGTCTGAGCGG--ATGACGGGAGCTTGTCTCTGAATCA 66  
QY 90 GAGCNGCGGACGGGTGAGTAATCTTAGGAATCTAGTGTGGGGATAGCTCGGG 149  
Db 67 G---CGGCGGACGGGTGAGTAATCGCTAGGAATCTGCTGTAGTGGGGACACAGCTCTC 123  
QY 150 GAAACTCGAATTAATACCGCATAGCT-CTAGCGGAGAAAGCAGGGGNTCAATTAGACCTTG 208  
Db 124 GAAAGGACGCTAATACCGCATAGCTCTTACGGGAGAAAGCAGGGGACCTTGGGGCTTG 183  
QY 209 CGCTATTAGTAGCCCTAAGTCGATAGTGTGGGTAAAGCCCTACCATGGCG 268  
Db 184 CGCTATTAGTAGCCCTAAGTCGATAGTGTGGGTAAAGCCCTACCATGGCG 243  
QY 269 ACATCTGTAGTCTGTAGAGGATGATCAGGCACACCGGGACTGAGACACGCGCCCGGA 328  
Db 244 ACATCTGTAGTCTGTAGAGGATGATCAGTCACTGGAATGAGACACGCTCCAGA 303  
QY 329 CT-CTACGGGAGGACGAGTGGGAAATTGGCAATGNGGGAACCCCTGATCCAGCCAT 387  
Db 304 CTCTACGGGAGGACGAGTGGGAAATTGGCAATGNGGGAACCCCTGATCCAGCCAT 363  
QY 388 GCGCGGTGTGAGAGGCGCTTTTGGTCTTAAGCACTTTAGCACTGAAGAGCTCT 447  
Db 364 GCGCGGTGTGAGAGGCGCTTTTGGTCTTAAGCACTTTAGCACTGAAGAGGCGAT 423  
QY 448 TCGGTTAATACCGGGGACGATGATCATTAGCTGAGAAATAGCACCCGGCTAACTCTGTGC 507

Db 424 TAACCTAATACGTAGTGTGTTGACGTTACCGACAGAAATAGCACCGGCTAACTCTGTGC 483  
QY 508 CAGCAGCGCGGTAATAACAGAGGGTGCAGCGTTAATTCGGAATTAATTCGGCGTAAAGCGA 567  
Db 484 CAGCAGCGCGGTAATAACAGAGGGTGCAGCGTTAATTCGGAATTAATTCGGCGTAAAGCGC 543  
QY 568 GCGTAGGTGCTTGAATGATGATGAAATCCCGGGCTTAACCTGGGAATCTGATCT 627  
Db 544 GCGTAGGTGCTTGAATGATGAAATCCCGGGCTTAACCTGGGAATCTGATCT 603  
QY 628 GAAACTCTTAGGCTAGAGTAGGTGAGAGGAAGTAGAATTTTCAAGTGTACGGTGAATG 687  
Db 604 AAACTGCAAGCTAGAGTAGGTGAGAGGTGAGGAATTTTCTGTGTACGGTGAATG 663  
QY 688 CGTAGAGATCTGAAGGAATACCGATGCGGAAGCAGCTTCTCTGGCATCATACTGACACTG 747  
Db 664 CGTAGATATAGGAAGGAACACCACTGCGGAAGCGCACCTGGACTGATCTGACACTG 723  
QY 748 AGCTCGAAGCGTGGGTAGCAAAACAGGATTAGATACCTCTGGTAGTCCACCGCGTAAAG 807  
Db 724 AGTGCAGAAAGCGTGGGGAGCAAAACAGGATTAGATACCTCTGGTAGTCCACCGCGTAAAG 783  
QY 808 ATGTCTACTAGTGTGGGTCCCTTGAAGACTTTAGTGACGCTAACGCAATAAGTAGA 867  
Db 784 ATGTCAACTAGCCGTTGGGAGCTTTGAGCTCTTAGTGGCGCAGCTAACGCAATTAAGTTGA 843  
QY 868 CCCTCTGGGAGTACGCGCCCAAGGTTAAACTCAAATGAATTAAGCGGGCCCGCACAA 927  
Db 844 CCCTCTGGGAGTACGCGCCCAAGGTTAAACTCAAATGAATTAAGCGGGCCCGCACAA 903  
QY 928 GCGGTGGAGCATGTGTTTAATTCGATGCAACCGGAGACCTTACCTGTCTTGCATATA 987  
Db 904 GCGGTGGAGCATGTGTTTAATTCGAGCAACCGGAAGAACCTTACACAGGCTTGCATC 963  
QY 988 CACAGAACTTGTAGAGATACGAGAGTGCTTCCGGGAATTTGTATACAGGTGTGTGATGG 1047  
Db 964 CAATGAATTTCCAGAGATGGATGGGTGCTTCCGGGAACATTGAGACAGGTGTGTGATGG 1023  
QY 1048 CTGTCTAGCTCGTGTGAGATGTGGGTAAAGTTCGCGCAACGAGCGCAACCTTGT 1107  
Db 1024 CTGTCTAGCTCGTGTGAGATGTGGGTAAAGTTCGCGTAAAGTTCGCGCAACGAGCGCAACCTTGT 1083  
QY 1108 CTTAGTTACACAGC-TCGCGGTGGAACTCTTAAGGATCTCCAGGATGACAACTGGAG 1166  
Db 1084 CTTAGTTACACAGCATAATGTGGGCACTCTTAAGGAGACTGCCGTGACAAACCGGAG 1143  
QY 1167 GAAGCGGGGACGACGCTCAAGTCAATCATGGCCCTTACGACAGGGGCTACACAGGTGTCTAC 1226  
Db 1144 GAAGTGGGATGACGCTCAAGTCAATCATGGCCCTTACGGCTTGGCTACACAGGTGTCTAC 1203  
QY 1227 AATGTAGGTACAGAGGCGAGCTACACAGGATGTGATGGAATCTCAAAAGGCTATCG 1286  
Db 1204 AATGTGTGTACAGAGGTTGCGAAGCGCGAGGTGGAGCTAATCCACAAAACCGGATCG 1263  
QY 1287 TAGTCCAGATTGAGTCTGCAACTCGACTCCATGAAGTAGGAATCGCTAGTAACTCGCGGA 1346  
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QY 1347 TCAGAAATGCCCGGTGAATACGTTCCCGGGCTTTGTACACACCGCGCTCACACCATGGG 1406  
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QY 1407 AGTTGATTGACACAGAGTGGTTAGCGTAA-CTTAGTAGAGGCGATCACACCGTGTGGT 1465  
Db 1384 AGTGGGTGTGACAGAGTAGTGTAGTCTAACTTTCGGGAGGACGGTTACACCGTGTGAT 1443  
QY 1466 CGATGACTGGGGTGAAGTGTAAAGTAGCCGTAGGGGAACCTTCGGCTTGCATCAC 1523  
Db 1444 TCATGACTGGGGTGAAGTGTGTAACAAGTAGCCGTAGGGAACTTCGGGCTGATCAC 1501

RESULT 7

US-09-951-720-1  
; Sequence 1, Application US/09951720  
; Patent No. 6635782  
; GENERAL INFORMATION:  
; APPLICANT: Canon Kabushiki Kaisha  
; TITLE OF INVENTION: Polyhydroxyalkanoate and Manufacturing Method Thereof  
; FILE REFERENCE: 4477001  
; CURRENT APPLICATION NUMBER: US/09/951,720  
; CURRENT FILING DATE: 2000-09-14  
; PRIOR APPLICATION NUMBER: JP 279900/2000  
; JP 378827/2000  
; JP 165238/2001  
; JP 165509/2001  
; JP 275063/2001  
; PRIOR FILING DATE: 2000-09-14  
; 2000-12-13  
; 2001-05-31  
; 2001-05-31  
; 2001-09-11  
; NUMBER OF SEQ ID NOS: 1  
; SEQ ID NO 1  
; LENGTH: 1501  
; TYPE: DNA  
; ORGANISM: Pseudomonas jessenii P161 strain.  
US-09-951-720-1

Query Match 72.0%; Score 1098.6; DB 4; Length 1501;  
Best Local Similarity 85.9%; Pred. No. 0; Mismatches 202; Indels 9; Gaps 6;  
Matches 1287; Conservative 0

QY 30 GCGGCGAGCTTAAACATGCAAGTCGAGCGGAAACGATGATGCTTCTATTAGCGCTC 89  
DB 9 GCGGCGAGCTTAAACATGCAAGTCGAGCGG--ATGACGGAGCTTCTCTGATTTCA 66

QY 90 GAGGCGCGAGCGGTGATGATTAATCTTAGGAACTACCTAGTAGTGGGGGATAGTCGGG 149  
DB 67 G---CGGCGGAGCGGTGATGATTAATCTTAGGAACTGCTTGGTGGGGGCAACGCTC 123

QY 150 GAACTCGAAATTAATACCGCATACGT-CTACGGGAGAAAGCAGGGGNTCATTAGACCTTG 208  
DB 124 GAAAGGAGCGTAAATACCGCATACGTCTACGGGAGAAAGCAGGGGACCTTGGGGCCTTG 183

QY 209 CGCTATTAGATGAGCCTAAGTCGATTAATCTAGTAGTGGTGGGTAAGGCTTACCATGGCG 268  
DB 184 CGCTATCAGATGAGCCTAGGTCGATTAATCTAGTAGTGGTGGGTAAGGCTTACCATGGCG 243

QY 269 ACGATCTGATGCTGATGAGGATGATCAGCACACCGGACCTGACACAGCGGCCGGA 328  
DB 244 ACGATCCGTAATCTGCTGAGAGGATGATCAGTCACTGGAACCTGAGACACGCTCCAGA 303

QY 329 CT-CTACGGGAGCGAGTGGGGAATATTGGACAATGNGGGAACCTGATCCAGCCAT 387  
DB 304 CTCCTACGGGAGCGAGTGGGGAATATTGGACAATGNGGGAACCTGATCCAGCCAT 363

QY 388 GCGCGGTGTGGAAGAGCGCTTTTGGTTGTAAGCACTTTTAAGCAGTGAAGAAGACTCT 447  
DB 364 GCGCGGTGTGGAAGAGCGCTTTTGGTTGTAAGCACTTTTAAGTGGGAGAGGCGAT 423

QY 448 TCGGTTAATACCGGGGAGATGACATTAAGTGTGAGATTAAGCAGCGGCTAATCTGTGC 507  
DB 424 TAACTTAATACCGTTAGTGTGAGGATTAAGCAGCGGCTAATCTGTGC 483

QY 508 CAGCAGCGCGGTAAATACAGAGGTCGAGCGTAAATCGGAATTAAGCAGCGGCTAAGCGA 567  
DB 484 CAGCAGCGCGGTAAATACAGAGGTCGAGCGTAAATCGGAATTAAGCAGCGGCTAAGCGC 543

QY 568 GCGTAGGTGCTTGAATAGTCAGATGTGAAATCCCGGGCTTAACTCGGGAATCTCATCT 627  
DB 544 GCGTAGGTGCTTGAATAGTCAGATGTGAAATCCCGGGCTTAACTCGGGAATCTCATCT 603

QY 628 GAACTGTAGCTAGTGTGAGAGGAGTGAATTTTCAAGTGTAGCGGTGAATG 687  
DB 604 AAACTGCAAGCTAGATGATGAGAGGTCGAGGATTTTCTGTGTAGCGGTGAATG 663

QY 688 CGTAGATCTGAAGGAATACCGATGGCGAAGGAGCTTCTGGCATCATACTGACACTG 747  
DB 664 CGTAGATATAGGAAGGAACACCGATGGCGAAGGAGCGACCATCTGGACTGATCTGACACTG 723

QY 748 AGGTCGAAAGCGTGGGTAGCAAAACAGATTAGATACCTCTGGTGTGTCACCGCGTAAACG 807  
DB 724 AGGTGCGAAAGCGTGGGAGCAAAACAGATTAGATACCTCTGGTGTGTCACCGCGTAAACG 783

QY 808 ATGTCTACTAGTCTGGTCCCTTGGAGCTTGTAGCGAGCTTGTAGCGAGCTTAAACGCAATAGTAGA 867  
DB 784 ATGTCAACTAGCTTGGAGCTTGTAGCTTGTAGTGGCGAGCTTAAACGCAATAGTAGA 843

QY 868 CCGCTGGGAGTACGCGCGCAAGTTAAACTCAAAATGAATTTGACGGGGGCCCGCACAA 927  
DB 844 CCGCTGGGAGTACGCGCGCAAGTTAAACTCAAAATGAATTTGACGGGGGCCCGCACAA 903

QY 928 GCGGTGAGCATGTGGTTTAAATTCGATGCAACGGAAGAACCTTACCTGCTGTGACATA 987  
DB 904 GCGGTGAGCATGTGGTTTAAATTCGAAAGCAACGGAAGAACCTTACCGAGGCTTGCATC 963

QY 988 CACAGAATCTTGTAGATACGAGAGTCCCTTCCGGAATTTGTATACAGGTGCTGCATGG 1047  
DB 964 CAATGAATCTTCCAGAGATGATGGTGCCTTCCGGAACATTGAGACAGGTGCTGCATGG 1023

QY 1048 CTGTCTGCTAGCTCGTGTGAGATGTTGGGTTAAAGTCCCGCAACGAGCGCAACCCCTTGT 1107  
DB 1024 CTGTCTGCTAGCTCGTGTGAGATGTTGGGTTAAAGTCCCGCAACGAGCGCAACCCCTTGT 1083

QY 1108 CCTTAGTTACCAAC-TTGCGGTGGGAATCTTAAGGATATGCGAGTGAACAACTGAG 1166  
DB 1084 CCTTAGTTACCAACGAGTAAATGTTGGGCACTCTTAAGGAGACTGCGCGTGAACAAACCGGAG 1143

QY 1167 GAAGCGGGAGCAGCTCAAGTCACTATGCGCCCTTACGACCGAGGCTACACAGTGTCTAC 1226  
DB 1144 GAAGTGGGAGTACGTCAGTCAATGTCATGCGCCCTTACGCGCTGGGCTACACAGTGTCTAC 1203

QY 1227 AATGCTAGTACAGAGGCGAGCTACAGCGCATGTGATCGCAATCTCAAAAGGCTATCG 1286  
DB 1204 AATGCTAGTACAGAGGCTTGCAGCGCGAGGTTGAGCTAATCCCAACAAACCGATCG 1263

QY 1287 TAGTCCAGATTGGAGTCTGCAACTCGACTCATGAAAGTGAAGTCTGCTAGTAAATCGCGGA 1346  
DB 1264 TAGTCCGAGTGCAGTCTGCAACTCGACTCGTGAAGTTCGGAATCGCTAGTAAATCGCGGA 1323

QY 1347 TCAGAAATGCGCGGTGAATACGTTCCCGGGCTTTGTACACACCGCGCTCACACCATCGG 1406  
DB 1324 TCAGAAATGCGCGGTGAATACGTTCCCGGGCTTTGTACACACCGCGCTCACACCATCGG 1383

QY 1407 AGTTGATTGCACCAAGAGTGGTTAGCCTAA-CTTAGTGAAGGCGGATCACACGGTGTGGT 1465  
DB 1384 AGTGGTTGCACCAAGAGTAGTCTAACCTTTCGGGAGGACGGTTACACCGGTGTGAT 1443

QY 1466 CGATGACTGGGGTGAAGTCTGTAACAGGTAGCGCTAGGGGAACCTGCGGCTGGATCAC 1523  
DB 1444 TCATGACTGGGGTGAAGTCTGTAACAGGTAGCGCTAGGGGAACCTGCGGCTGGATCAC 1501

## RESULT 8

US-10-411-319-1  
; Sequence 1, Application US/10411319  
; Patent No. 6649381  
; GENERAL INFORMATION:  
; APPLICANT: Canon Inc.  
; TITLE OF INVENTION: Polyhydroxynate, Method For Production Thereof And Microorganisms  
; FILE REFERENCE: In The Same  
; FILE REFERENCE: 03500.01500.1  
; CURRENT APPLICATION NUMBER: US/10/411,319  
; CURRENT FILING DATE: 2003-04-11  
; PRIOR APPLICATION NUMBER: US 09/748,205  
; PRIOR FILING DATE: 2000-12-27  
; NUMBER OF SEQ ID NOS: 1  
; SOFTWARE: PatentIn version 3.1

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; SEQ ID NO 1
; LENGTH: 1501
; TYPE: DNA
; ORGANISM: Pseudomonas jessenii 161 strain
US-10-411-319-1

Query Match      72.0%; Score 1098.6; DB 4; Length 1501;
Best Local Similarity 85.9%; Pred. No. 0;
Matches 1287; Conservative 0; Mismatches 202; Indels 9; Gaps 6;

Qy 30 GCGCGCAGGCTTAACACATGCAAGTCGAGCGGAACGATAGCTTGTCTATTAGGCGTC 89
Db 9 GCGCGCAGGCTTAACACATGCAAGTCGAGCGG--ATGACGGGAGCTTGTCTCTGAAATCA 66
Qy 90 GAGCNGCGGACGGGTGAGTAATCTTAGGAATCTACTAGTAGTGGGGGATAGCTCGGG 149
Db 67 G---CGGCGGACGGGTGAGTAATCTAGGAATCTGCTGTGTAGTGGGGGACACAGCTCTC 123
Qy 150 GAACTCGAATTATACCGCATAGT-CTACGGGAGAAACGAGGGNTCTATTAGACCTTG 208
Db 124 GAAAGGACGCTAATACCGCATAGTCTCTACGGGAGAAACGAGGGACCTTTCGGGCGCTTG 183
Qy 209 CGCTATTAGATGACCTAAAGTCGATAGCTAGATGCTGGGTAAAGGCTTACCATGGCG 268
Db 184 CGCTATCAGATGACCTAGTTCGATAGCTAGTGTGGTGAAGTAATGGCTCACCAAGCG 243
Qy 269 ACATCTGTAGCTGTCTGAGAGGATGATACGCCACACCGGGAATGAGACACGCGCCCGGA 328
Db 244 ACATCTGTAGCTGTCTGAGAGGATGATCAGTCACACCTGGAACTGAGACACGCTCCAGA 303
Qy 329 CT-CTACGGGAGGACAGATGGGGAATATTGGCAATGNGGGAAACCTGATCCAGCCAT 387
Db 304 CTCCTACGGGAGGACAGATGGGGAATATTGGCAATGNGGGAAAGCTGATCCAGCCAT 363
Qy 388 GCGCGGTGTGTGAAGAAGGCTTTTGGTTGTAAAGCACTTTAAGCAGTGAAGAGACTCT 447
Db 364 GCGCGGTGTGTGAAGAAGGCTTTCGGATTTGTAAGCACTTTAAGTTGGGAGGAAGGCGAT 423
Qy 448 TCGGTTAATACCGGGACGATGACATTAAGTCAGAAATAGCAACCGGCTTAATCTGTGC 507
Db 424 TAACCTAATACGTTAGTGTGTTTGAAGTACCGAGAAATAGCAACCGGCTTAATCTGTGC 483
Qy 508 CAGCAGCGCGGTAATACAGAGGTCGAAGGCTTAATCGGAATTAATCGGCGTAAAGCGGA 567
Db 484 CAGCAGCGCGGTAATACAGAGGTCGAAGGCTTAATCGGAATTAATCGGCGTAAAGCGG 543
Qy 568 GCGTAGTGGCTTCAATAGTCAGATGTGAATCCCGGGCTTTAACCCTGGGAATGCAATCT 627
Db 544 GCGTAGTGGCTTCTTAAGTTGGATGTGAAGCCCGGGCTCAACCTGGGAATGCAATTC 603
Qy 628 GAACTGTTAGGCTAGGTCAGAGGGAAGTAGAATTCAGGTGTAGGCTGAAGT 687
Db 604 AAAAAGTACAGCTAGAGTATGAGAGGCTGAGGAAATTCCTGTGTAGCGGTGAAGT 663
Qy 688 CGTAGAGATCTGAAGGAATACCGATGGCGAAGGAGCTTCTTGGCATCATACTGACACTG 747
Db 664 CGTAGATATAGGAAGGAACACCACTGGGGAAGGCGCACCACTGGAATGATGACACTG 723
Qy 748 AGGCTCGAAACGCTGGGTAGCAAAACAGATTAAGTACCTGGTGTAGTCCACCGCGTAAACG 807
Db 724 AGGTGCGAAACGCTGGGAGCAAAACAGATTAAGTACCTGGTGTAGTCCACCGCGTAAACG 783
Qy 808 ATGCTACTAGTCTGGTCCCTTGGAGCTTATGACGACGCTACGCAATTAAGTGA 867
Db 784 ATGCTACTAGTCTGGGAGCTTGGAGCTTATGACGACGCTACGCAATTAAGTGA 843
Qy 868 CCGCTCGGAGTACGCGCGCAAGGTTAAACTCAAAATGAATGACGGGGGCGCGCAAA 927
Db 844 CCGCTCGGAGTACGCGCGCAAGGTTAAACTCAAAATGAATGACGGGGGCGCGCAAA 903
Qy 928 GCGGTGAGCATGTGGTTTAAATTCGATGCAACGGGAAGACCTTACCTGGTCTTGACATA 987
Db 904 GCGGTGAGCATGTGGTTTAAATTCGATGCAACGGGAAGACCTTACCTGGTCTTGACATA 963
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Qy 988 CACAGAATCTTGTAGAGATACGAGAGTGCCCTTCGGGAATTTGTATACAGTGTGATGG 1047
Db 964 CAATGAACCTTTCAGAGATGGATGGGTGGCTTCGGGAACATTTGAGACAGGTGTGATGG 1023
Qy 1048 CTGTCTGTCAGCTCGTGTGAGATGTTGGGTTAAGTCCGCAACAGAGCGCAACCCCTTGT 1107
Db 1024 CTGTCTGTCAGCTCGTGTGAGATGTTGGGTTAAGTCCGTAACAGAGCGCAACCCCTTGT 1083
Qy 1108 CTTAGTTACAGCAC-TTCGGGTGGGAATCTTAAGGATATCTCCAGTGTGACAACTGGAG 1166
Db 1084 CTTAGTTACAGCACGTAATGTTGGGCACTCTTAAGGAGACTGCCGTGACAAACCGGAG 1143
Qy 1167 GAAGCGGGGACAGCTCAAGTCAATGATGATGATGATGATGATGATGATGATGATGATGAT 1226
Db 1144 GAAGGTGGGATGACGTCAGTCAAGTCAATGATGATGATGATGATGATGATGATGATGATGAT 1203
Qy 1227 AATGTTAGGTACAGAGGCGAGCTACACAGGATGTGATGATGATGATGATGATGATGATGATGAT 1286
Db 1204 AATGTTAGGTACAGAGGCGAGTTCGCAAGCGGAGGTGAGTAAATCCACAAACCGGATCG 1263
Qy 1287 TAGTCCAGATTTGAGTCTGCAACTCCATCCATGAAAGTAGGAATCGCTAGTAATCGCGGA 1346
Db 1264 TAGTCCAGATTTGAGTCTGCAACTCCATCCATGAAAGTAGGAATCGCTAGTAATCGCGGA 1323
Qy 1347 TCAGATGCGCGGTGAATACGTTCCGGGCTTTGTACACACCGCGCTCACACCATGGG 1406
Db 1324 TCAGATGCGCGGTGAATACGTTCCGGGCTTTGTACACACCGCGCTCACACCATGGG 1383
Qy 1407 AGTTGATTGACACAGAGTGGTTAGCTAA-CTTAGTGAGGGCGATCACCAACGCTGTGGT 1465
Db 1384 AGTTGATTGACACAGAGTGGTTAGCTAA-CTTAGTGAGGGCGATCACCAACGCTGTGGT 1443
Qy 1466 CGATGCTGGGTGAAGTCTGAACAGGTAGCGGTAGGGGAACCTCGGCTGATCAC 1523
Db 1444 TCATGCTGGGTGAAGTCTGAACAGGTAGCGGTAGGGGAACCTCGGCTGATCAC 1501
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## RESULT 9

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US-10-105-305-1
; Sequence 1, Application US/10105305
; Patent No. 6777153
; GENERAL INFORMATION:
; APPLICANT: CANON KABUSHIKI KAISHA
; TITLE OF INVENTION: POLYHYDROXYALKANOATE CONTAINING UNIT WITH THIENYL STRUCTURE IN THE
; TITLE OF INVENTION: CHAIN, PROCESS FOR ITS PRODUCTION, CHARGE CONTROL AGENT, TONER B.
; TITLE OF INVENTION: TONER WHICH CONTAINS THIS POLYHYDROXYALKANOATE, AND IMAGE-FORMING
; TITLE OF INVENTION: IMAGE-FORMING APPARATUS WHICH MAKE USE OF THE TONER
; FILE REFERENCE: CPO16309
; CURRENT APPLICATION NUMBER: US/10/105,305
; CURRENT FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: JP 2001-090026, JP 2001-133551
; PRIOR FILING DATE: 2001-3-27, 2001-4-27
; NUMBER OF SEQ ID NOS: 1
; SEQ ID NO 1
; LENGTH: 1501
; TYPE: DNA
; ORGANISM: Pseudomonas jessenii 161 strain.
US-10-105-305-1
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Query Match      72.0%; Score 1098.6; DB 4; Length 1501;
Best Local Similarity 85.9%; Pred. No. 0;
Matches 1287; Conservative 0; Mismatches 202; Indels 9; Gaps 6;

Qy 30 GCGCGCAGGCTTAACACATGCAAGTCGAGCGGAACGATAGCTTGTCTATTAGGCGTC 89
Db 9 GCGCGCAGGCTTAACACATGCAAGTCGAGCGG--ATGACGGGAGCTTGTCTCTGAAATCA 66
Qy 90 GAGCNGCGGACGGGTGAGTAATCTTAGGAATCTACTAGTAGTGGGGGATAGCTCGGG 149
Db 67 G---CGGCGGACGGGTGAGTAATCTAGGAATCTCCCTGGTGTAGTGGGGGACACAGCTCTC 123
Qy 150 GAAACTCGAATTAAATACCGCATAGT-CTACGGGAGAAACGAGGGNTCTATTAGACCTTG 208
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Db 338 ACUUCUACGGGAGCAGAGUGGGGAAUUAUUCACAAUUGGGCGCAAGCCUGAUGCAGCCA 397  
Qy 387 TCCCGCGTGTGTGAAGAGCGCTTTTGGTTGTAAAGACTTTAAGCAGTGAAGAGACTC 446  
Db 398 UCCCGGUGUAGAGAGAGCCUUCGGGUGUAAAGUACUUCACGGGGAGAGAGGAG 457  
Qy 447 TTCGGTTAATACCCGGGACAGATGATTAAGTGTGAGATAAGCACCAGCTTCTGTG 506  
Db 458 UAAAGUUAUACCUUUGCUAUGAUGUACCCGAGAGAGACCCGCGUAAUCCUGUG 517  
Qy 507 CCAGCAGCGCGGTAAACAGAGGGTGAAGGTTAATCGGAATTAAGTGGGGTAAAGG 566  
Db 518 CCAGCAGCGCGGUAUACCGAGGGUGCAAGCGUUAUUGGGAUUAUUGGCGUAAAGCG 577  
Qy 567 AGCGTAGGTGGCTGATAGTCAAGTGTGAATGCCGGCTTAACCTGGGAATCGATC 626  
Db 578 CACGAGCGGUGUUAAGUCAGUGUAGUAAUCCCGGGCUACACCTUGGGAUUGCAUC 637  
Qy 627 TGAATCTGTAGGTAGGTAGGTGAGAGGAAGTAGAATTTACGTTGTAGCGTGAAT 686  
Db 638 UGAUACUGGCAAGCUUGAGUCUGUAGAGGGGGUAGAAUUCAGGUGUAGCGGUGAAU 697  
Qy 687 GCGTAGAGATCTGAAGGATACCGATGCGAGGAGCTTCTGGCATCATCTACACT 746  
Db 698 GCGUAGAUUGGAGGAAUACCGGUGCGAAGCGGCCCGGAGCAAGACUGACGCU 757  
Qy 747 GAGGCTCGAAAGCGTGGGTAGCAAAACAGGATTAGATACCTGGTAGTCCACGCGTAAAC 806  
Db 758 CAGGUGCGAAGCGUGGGGAGCAAAACAGGAUUAUCCUGUAGUACCGCGCUAAAC 817  
Qy 807 GATGCTACTAGTCTGGTGGTCCCTTTAGGAGCTTAGTGACGAGCTAACGCAATAGTAG 866  
Db 818 GAUGUGCAUUGGAGGUGUUGCCUUGAGGCGUGGCUUCGCGAGCUAACGCGUUAAGUG 877  
Qy 867 ACCGCTGGGAGTACGCGCGCAAGGTTAAACTCAATGAATTCACGCGGGCGCGACA 926  
Db 878 ACCGCGGGGAGUACGCGCGCAAGGUAUAAACUCAAAUGAAUUGACGGGGCGCGACA 937  
Qy 927 AGCGGTGAGCATGTGTTAATTCGATGCAACGCGAAGAACCTTACCTGGTCTTGACAT 986  
Db 938 AGCGGUGAGUUGGUGUUAUUCGUAUGCAACGCGAAGAACCUUACUGGUGUAGAU 997  
Qy 987 ACACAGAATCTTGTAGATACAGAGTGCCTTCGGGAATTGTATACAGGTGTGCAATG 1046  
Db 998 CCACGGAUUAUUCAGAGAGAAUGUGCCUUCGGAACCGUGAGACAGGUGUGCAUG 1057  
Qy 1047 GCTGTCGTAGTCTGTCGTGAGATCTTGGTTAAGTCCGCAACGAGCGCAACCTTG 1106  
Db 1058 GCGUGCGUACGUGUGUUGAAUUGUGGUAAGUCCCGCAACGAGCGCAACCCUUA 1117  
Qy 1107 TCCTTTAGTTACAGCACTTCGGGTGGGAATCTAAGGATCTGCCAGTGAACAACTGGAG 1166  
Db 1118 UCCUUGUUGCAGCGGUGCGCGCGGAACUCUAAAGGAGACUGCCAGUUAUACUGGAG 1177  
Qy 1167 GAAGCGGGGACGCTCAAGTCAATGCGCCCTTACGACCAAGGCTACACACGCTGCTAC 1226  
Db 1178 GAAGUGGGAGUAGCUCAAGUACUAGUGCCCUUACGACGAGGCGUACACAGGUGUAC 1237  
Qy 1227 AATGTTAGTACAGAGGCGAGTACACAGCGATGTGATCGGATCTCAAAAGCCTATCG 1286  
Db 1238 AAUGCGCAUACAAAGAGAAGCGACUUCGCGAGAGCAAGCGACCUCAUAAAGUGCGUG 1297  
Qy 1287 TAGTCCAGATTGAGTCTGCAACTCGACTCCATGAAGTAGGAATCGCTAGTAATCGCGGA 1346  
Db 1298 UAGUCCGAUUGGAGUUGCAACUCGACUCCUAAUGAAGUGGAUUCGUGAUAUUGUGGA 1357  
Qy 1347 TCAGAAATCCCGGTTGAATACGTTCCCGGGCTTGTACACACCGCCCGCTACACCATGGG 1406  
Db 1358 UCAGAAUCCGCGGUAUACGUUCCCGGGCCUUGUACACACCGCCCGUACACACCAUGGG 1417  
Qy 1407 AGTTGATTGACCAAGAGTGTGTAGCTTAACTTGTAGTGGGCGATACACAGGTGTGTT 1465  
Db 1418 AGUGGUGUAGAAAGUAGUAGUUAUCCUUCGGGAGGCGGCUUACCAUUGUGAU 1477

Qy 1466 CGATCACTGGGTGAAGTCTGTAAACAAAGGTAGCCGTAGGGAACTTGGCTGCATCACCT 1525  
Db 1478 UCAUGACUGGGUGAGUAGUUAACAAAGUACCGUAGGGGAACCUUGCGUUGAUCACU 1537  
Qy 1526 C 1526  
Db 1538 C 1538

RESULT 12  
US-09-726-774-3  
; Sequence 3, Application US/09726774  
; Patent No. 6677153  
; GENERAL INFORMATION:  
; APPLICANT: Iversen, Patrick L.  
; TITLE OF INVENTION: Anticibense Antibacterial Method and  
; TITLE OF INVENTION: Composition  
; FILE REFERENCE: 0450-0032.30  
; CURRENT APPLICATION NUMBER: US/09/726,774  
; PRIOR FILING DATE: 2000-11-29  
; PRIOR APPLICATION NUMBER: US 60/168,150  
; PRIOR FILING DATE: 1999-11-29  
; NUMBER OF SEQ ID NOS: 139  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 1467  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa  
US-09-726-774-3

Query Match 70.2%; Score 1070.8; DB 4; Length 1467;  
Best Local Similarity 85.9%; Pred. No. 0;  
Matches 1233; Conservative 0; Mismatches 199; Indels 4; Gaps 4;  
Qy 95 GCCGACCGGTGAGTAACTTAGAATCTACCTAGTAGTGGGATAGCTCGGGGAAC 154  
Db 29 GCGGACCGGTGAGTAACTTAGAATCTACCTAGTAGTGGGATAGCTCGGGGAAC 88  
Qy 155 TCGAATTAATACCCATACGT-CTACGGGAGAAAGAGGGGNTATTAGACTTGGCTA 213  
Db 89 GAACGCTAATACCCATACGTCTACGGGAGAAAGAGGGGACCTTCGGGCTTGGCTA 148  
Qy 214 TTAGATAGCCCTAAGTTCGATTAGTCTAGATGGTGGGTAAGGCTACATGGCGACGAT 273  
Db 149 TCAGATAGCCCTAGTTCGATTAGTCTAGTGGTAAAGGCTACCAAGGCGACGAT 208  
Qy 274 CTGTAGTGTCTGAGAGGATGATCAGCCACACCGGGACTGAGACACCGGCGGACT-CT 332  
Db 209 CCGTAACTGGTCTGAGAGGATGATCAGTCACTGGAACCTGAGACACCGTCCAGACTCT 268  
Qy 333 ACGGAGGCGACGAGTGGGGAATATTGGACATGNGGAAACCTGATCCAGCCATGCCGC 392  
Db 269 ACGGAGGCGACGAGTGGGGAATATTGGACATGNGGAAACCTGATCCAGCCATGCCGC 328  
Qy 393 GTGTGTGAAGAAGCGCTTTTGGTTGTAAAGCACTTTAAGCAGTGAAGAAGACTCTTCGT 452  
Db 329 GTGTGTGAAGAAGCGCTTTTGGTTGTAAAGCACTTTAAGTGGGAGGAGGCGATTAACC 388  
Qy 453 TAATACCGGGGACGATGACATTAAGTGTGAGATAAGCAACCGGCTTAATCTGTGCGACA 512  
Db 389 TAATACCGTTAGTTTGGACCTTACCGACAGAAATAAGCACCGGCTTAATCTGTGCGACA 448  
Qy 513 GCGCGGTAAATACAGGGTCAAGCGTTTATCGAATTAATCGGCTTAAAGCGGAGCGCTA 572  
Db 449 GCGCGGTAAATACAGGGTCAAGCGTTTATCGAATTAATCGGCTTAAAGCGGAGCGCTA 508  
Qy 573 GGTGCTTGAATAGTCAAGTGAATCCCGGGCTTAACTGGGAACTGATCTGGAAC 632  
Db 509 GGTGCTTGAATAGTGAATGAAAGCCCGGCTCAACTGGGAATGATCTGGAAC 568  
Qy 633 TGTTAGGCTAGAGTAGGTGAGAGGAGTGAATTTTCAAGTGTAGCGGTGAATTCGGTAG 692



Db 569 TGGCAAGCTAGATATGGCAGAGGGTGTGGATTTCTCTGTGTAGCGGTGAATGCGTAG 628  
Qy 693 AGATCTGAAGGAATACCGATGGCGAAGCGAGCTTCTTGGCATCATCTGACACTGAGGCT 752  
Db 629 ATATAGGAAGGAACACCAAGTGGCGAAGCGACCACTGGGCTAATCTGACACTGAGGTG 688  
Qy 753 CGAAAGCGTGGGTAGCAACAGAGATTAGATACCTGTGTAGTCCACGCGGTAAACGATGTC 812  
Db 689 CGAAAGCGTGGGAGCAACAGAGATTAGATACCTGTGTAGTCCACGCGGTAAACGATGTC 748  
Qy 813 TACTAGTCTGTGGTCCCTTGGAGACTTAGTGACGCACTAAACGCAATAAGTAGACCGCC 872  
Db 749 GACTAGCGTGGGATCTTGGATCTTGGAGCTTAGTGGCGCAGCTAAACGATTAAAGTCGACCGCC 808  
Qy 873 TGGGAGTACGCGCGCAAGGTTAAACTCAAAATGAATTTGACGCGGCGCCGCAACGCGGT 932  
Db 809 TGGGAGTACGCGCGCTAGGTAAACTCTAATGAATTTGACGCGGCGCCGCAACGCGGT 868  
Qy 933 GGAGCATGTGTTAAATTCGATGCAACGCGAAGCACTTACCTGGTCTTGACATACACAG 992  
Db 869 GGAGCATGTGTTAAATTCGAGCAACGCGAAGCACTTACCGGCTTGACATGCGAGAG 928  
Qy 993 AATCTGTAGAGATACGAGAGTGCCTTTCGGGAATTTGTATACAGGTGCTGATGGCTGTC 1052  
Db 929 AACTTTCAGAGATGATTTGGTCTTTCGGGAATTTGTATACAGGTGCTGATGGCTGTC 988  
Qy 1053 GTAGCTCTGTGCTGATGATTTGGGTTAAGTCCGCAACGAGCGCAACCTTGTCTCTTA 1112  
Db 989 GTAGCTCTGTGCTGATGATTTGGGTTAAGTCCGCTTAACGAGCGCAACCTTGTCTCTTA 1048  
Qy 1113 GTTACCAAGCAC-TTCGGGTGGGAATCTTAAGGATGACTGCGAGTGACAAATCGAGGAAGG 1171  
Db 1049 GTTACCAAGCACGTTAAGGTGGGCACTCTAAGGAGACTGCGCGGTGACAAACGAGGAGG 1108  
Qy 1172 CGGGAGCAGCTCAAGTCAATGCGCCCTTACGACAGGCTACACAGGTGCTACAATGG 1231  
Db 1109 TGGGAGTACGCTCAAGTCAATGCGCCCTTACGCGCTGAGCTACACAGGTGCTACAATGG 1168  
Qy 1232 TAGGTACAGAGGCGAGCTACACAGGATGTGATCGGAATCTCAAAAGCTATCGTAGTC 1291  
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Db 1229 CGGATCGAGTCTGCAACTCGACTCGTGAAGTCGGAATCGCTAGTAATCGTGAATCAGA 1288  
Qy 1352 ATGCCCGCGTGAATPACGTTCCCGGCGCTTGTACACACCGCGCGTACACCATGGAGTTG 1411  
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Qy 1412 ATTGCACAGAGTGGTTAGCTTAA-CTTAGTAGGGGCGATCACCAGGTGTGTCGATG 1470  
Db 1349 GTTGTCTCAGAAAGTAGCTAGTCTAACTTCCGGGGGACGTTACCAAGGAGGTATTCTATG 1408  
Qy 1471 ACTGGGTGAAGTCTGAACAGGTAGCGGTAGGGGAACCTTGGGCTGGATCACCTC 1526  
Db 1409 ACTGGGTGAAGTCTGAACAGGTAGCGGTAGGGGAACCTTGGGCTGGATCACCTC 1464

## RESULT 13

US-08-757-653-158

; Sequence 158, Application US/08757653

; Patent No. 5843669

; GENERAL INFORMATION:

; APPLICANT: Kaiser, Michael W.

; APPLICANT: Lyamichev, Victor I.

; APPLICANT: Lyamichev, Natasha

; TITLE OF INVENTION: Cleavage Of Nucleic Acid Using

; TITLE OF INVENTION: Thermostable FEN-1 Endonucleases

; NUMBER OF SEQUENCES: 190

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Medlen &amp; Carroll, LLP

; STREET: 220 Montgomery Street, Suite 2200

; CITY: San Francisco  
; STATE: California  
; COUNTRY: United States Of America  
; ZIP: 94104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/757,653  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ingolia, Diane E.  
; REGISTRATION NUMBER: 40,027  
; REFERENCE/DOCKET NUMBER: FORS-02565  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 705-8410  
; TELEFAX: (415) 397-8338  
; INFORMATION FOR SEQ ID NO: 158:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1542 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; US-08-757-653-158

Query Match 70.1%; Score 1069.2; DB 2; Length 1542;

Best Local Similarity 83.7%; Pred. No. 0;

Matches 1256; Conservative 0; Mismatches 241; Indels 4; Gaps 4;

Qy 30 GCGGCGAGGCTTAACATGCAAGTCGAGCGGAAC-GATGATAGCTGTGTTATTAGCGGT 88  
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Qy 89 CGAGCGCGGCGAGGCTGAGTAACTCTTAGGAATCTACCTAGTAGTGGGGGATAGCTCGG 148  
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Db 158 GGAACCGGTAGTAAATACCGCATAAACGTCGCAAGACCAAGAGGGGACCTTCGGGCGTC 217  
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Qy 328 ACT-CTACGGGAGCGAGCTAGTGGGGAATATTTGGAACAATGNGGGAACCTTGATCCAGCCA 386  
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Qy 387 TGGCGGTGTGTGAAGAGGCTTTTGGTTTAAAGCACTTTTAAAGCACTGAGCAAGAGACTC 446  
Db 398 TGGCGGTGTGTGAAGAGGCTTTTGGTTTAAAGCACTTTTAAAGCACTGAGCAAGAGGAG 457  
Qy 447 TCGGTTAATACCCGGGAGCGATGACATTAAGCTGCAAGATAAGCACCGGCTAACTCTGTG 506  
Db 458 TAAAGTTAATACCTTTGCTCATTTAGCGTTACCCGCAAGAGAACCGGCTAACTCGTG 517  
Qy 507 CCAGCAGCCCGGTAAATACAGAGGTTGCAAGCGTTAATCGGAATTAATCTGGCGGTAAAGCG 566  
Db 518 CCAGCAGCCCGGTAAATACAGAGGTTGCAAGCGTTAATCGGAATTAATCTGGCGGTAAAGCG 577  
Qy 567 AGCGTAGGTGCTTGAATAGTCAGATGTAAGTCCCGGCTTAACTCCCGGCTGATC 626  
Db 578 CAGCAGCGGCTTTGTTTAAAGTCAAGTGTGAATCCCGGCTCAACTGGAACCTGATC 637





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Qy 807 GATGCTACTAGTCTGGTCCCTTGGAGGACTTAGTACCGCAGCTACGCAATAAGTAG 866  
Db 818 GAUGUGGAGUUGGAGUUGGUGCCUUGAGGCGUGGCUUCCGGAGCUAACGCGUUAAGUCG 877  
Qy 867 ACCGCTGGGAGTACCGCCGCAAGGTTAAACTCAAATGAATTCAGCGGGGCCCGGCACA 926  
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Db 1478 UCAUGACUGGGGUAAGUUGUUAACAGGUAAACCGUAGGGGACCUCCGCGGUGUUGAUCU 1537  
Qy 1526 C 1526  
Db 1538 C 1538

## RESULT 15

US-08-520-946-158  
; Sequence 158, Application US/08520946  
; Patent No. 6372424  
; GENERAL INFORMATION:  
; APPLICANT: BROW, MARY ANN D.  
; APPLICANT: LYAMICHEV, VICTOR I.  
; TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF  
; NUMBER OF SEQUENCES: 160  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MEDLEN & CARROLL  
; STREET: 220 MONTGOMERY STREET, SUITE 2200

; CITY: SAN FRANCISCO  
; STATE: CALIFORNIA  
; COUNTRY: UNITED STATES OF AMERICA  
; ZIP: 94104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/520,946  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CARROLL, PETER G.  
; REGISTRATION NUMBER: 32,837  
; REFERENCE/DOCKET NUMBER: FORS-01756  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 705-8410  
; TELEFAX: (415) 397-8338  
; INFORMATION FOR SEQ ID NO: 158:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1542 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; US-08-520-946-158

Query Match 70.1%; Score 1069.2; DB 3; Length 1542;  
Best Local Similarity 83.7%; Pred. No. 0;  
Matches 1256; Conservative 0; Mismatches 241; Indels 4; Gaps 4;  
Qy 30 GCGCGCAGGCTTAAACATGCAAGTCGAGCGGAAC-GATGATAGCTTGTCTATTAGCGGT 88  
Db 38 GCGCGCAGGCTTAAACATGCAAGTCGAGCGGAACGATGATAGCTTGTCTATTAGCGGT 97  
Qy 89 CGAGCGCGCGGCGGTGAGTAACTCTTAGGAATCTACCTAGTAGTGGGGGATAGTCTGG 148  
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Qy 567 AGCGTAGGTGGCTTGTAAAGTGCAGATGTGAAATCCCCCGGGCTTAACTCTGGAACTGCATC 626  
Db 578 CAGCGAGGCGGTTTGTGTAAGTGCAGATGTGAAATCCCCCGGGCTCAACTCTGGAACTGCATC 637



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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: April 12, 2005, 04:59:42 ; Search time 1132.89 Seconds  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters: 11230502

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA:\*

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- 20: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq:\*
- 21: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*
- 22: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1098.6	72.0	1501	9	US-09-745-476-1
3	1098.6	72.0	1501	9	US-09-821-018-5
4	1098.6	72.0	1501	9	US-09-748-205-1
5	1098.6	72.0	1501	9	US-09-793-920A-1
6	1098.6	72.0	1501	9	US-09-951-720-1
7	1098.6	72.0	1501	10	US-09-791-610-1
8	1098.6	72.0	1501	14	US-10-218-519-5
9	1098.6	72.0	1501	14	US-10-266-787-5
10	1098.6	72.0	1501	14	US-10-252-518-5
11	1098.6	72.0	1501	14	US-10-105-305-1

12	1098.6	72.0	1501	15	US-10-133-404A-1
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14	1098.6	72.0	1501	17	US-10-411-319-1
15	1098.6	72.0	1501	17	US-10-649-646-1
16	1098.6	72.0	1501	17	US-10-603-996-1
17	1098.6	72.0	1501	18	US-10-827-670-1
18	1098.6	72.0	1501	18	US-10-007-725-5
19	1090.4	71.5	1494	13	US-09-737-297-4
20	1073.8	70.4	1481	9	US-09-726-774-3
21	1070.8	70.2	1467	9	US-09-027-439-7
22	1070.6	70.2	1467	18	US-10-719-633-3
23	1070.2	70.1	1541	9	US-10-361-002-6
24	1070.2	70.1	1542	18	US-10-361-004-6
25	1070.2	70.1	1534	16	US-10-029-397A-35
26	1069.2	70.1	1542	10	US-09-940-925A-158
27	1069.2	70.1	1542	10	US-09-941-193A-158
28	1069.2	70.1	1542	14	US-10-061-071-33
29	1066.2	69.9	10903	18	US-10-612-224-1
30	1065.2	69.8	11918	18	US-10-612-224-2
31	1065.2	69.8	13278	18	US-10-612-224-3
32	1062.6	69.6	1541	9	US-09-726-774-2
33	1062.6	69.6	1541	18	US-10-719-633-2
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35	1058.2	69.3	1549	9	US-09-912-020-242
36	1058.2	69.3	1549	9	US-09-912-020-402
37	1058.2	69.3	1549	18	US-10-771-241-89
38	1058.2	69.3	1549	18	US-10-771-241-242
39	1058.2	69.3	1549	18	US-10-771-241-402
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ALIGNMENTS

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US-10-672-787-41/c  
; Sequence 41, Application US/10672787  
; Publication No. US20040067554A1  
; GENERAL INFORMATION:  
; APPLICANT: LAGACE, Robert, E.  
; APPLICANT: PATTERSON, Chandra  
; APPLICANT: BERG, Kim, L.  
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF MORAXELLA CATARRHALIS GENOME  
; FILE REFERENCE: ELITRA.025C1  
; CURRENT APPLICATION NUMBER: US/10/672.787  
; CURRENT FILING DATE: 2003-09-26  
; PRIOR APPLICATION NUMBER: 09/596,002  
; PRIOR FILING DATE: 2000-06-16  
; NUMBER OF SEQ ID NOS: 41  
; SOFTWARE: PERL Program  
; SEQ ID NO 41  
; LENGTH: 269223  
; TYPE: DNA  
; ORGANISM: Moraxella catarrhalis  
US-10-672-787-41

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Best Local Similarity	90.6%	Pred. No. 0;		
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Db      |||||
QY 508 CAGCAGCCGCTAATACAGAGGTCGAAGCTTAAATCGGAATTAAGTGGGCTAAAGCGA 567
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QY 568 GCGTAGGTGGCTGTGTAAGTACAGATGTGAAATCCCGGCTTAACTGGGAATCTCATCT 627
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Db      |||||
QY 628 GAACTGTTAGCTAGAGTAGGTGAGAGGGAAGTAGAATTTTCAGGTGTAGCGGTGAAATG 687
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QY 604 AAACTGACAGCTAGAGTAGGTGAGAGGTCGTTGGAATTTCTGTGTAGCGGTGAAATG 663
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QY 688 CGTAGAGATCTGAAGGAATACCGATGCGGAAGGACGCTTCTGGCATATATCTGACATG 747
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; Sequence 5, Application US/09821016
; Patent No. US2001004692A1
; GENERAL INFORMATION:
; APPLICANT: CANON INC.
; TITLE OF INVENTION: Polyhydroxyalkanoate Synthase and Gene Encoding the Same Enzyme
; FILE REFERENCE: 4051021
; CURRENT APPLICATION NUMBER: US/09/821,016
; CURRENT FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Microsoft Word
; SEQ ID NO 5
; LENGTH: 1501
; TYPE: DNA
; ORGANISM: Pseudomonas jessenii P161; BP-7376
; FEATURE:
US-09-821-016-5
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Query Match          72.0%; Score 1098.6; DB 9; Length 1501;
Best Local Similarity 85.9%; Pred. No. 1.2e-288;
Matches 1287; Conservative 0; Mismatches 202; Indels 9; Gaps 6;

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Db      |||||
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QY 67 G---CGGCGGAGCGGTGAGTAACTCGCTAGGAATCTGCTGTAGTGGGGGCAACGCTC 123
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Db      |||||
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QY 304 CTCCTACGGGAGGACGAGTGGGGAATATTGGACAATGNGGGGAACCTGATCCAGCCAT 363
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QY 388 GCCCGGTGTGTGAAGAGGCGCTTTTGGTTGTAAAGCACTTTTAAAGCAGTGAAGAAGACTCT 447
Db      |||||
QY 364 GCCCGGTGTGTGAAGAGGCTCTTCGGATTGTAAAGCACTTTTAAAGTGGGAGGAGGCGAT 423
Db      |||||
QY 448 TCGGTTAATACCCGGGACGATGATACATATTAGTCGAGAAATAGACACCGGCTAACTCTGTGC 507
Db      |||||
QY 424 TAACTTAATACGTTAGTGTGTTTGTAGCTTACCGACAGAAATAGACACCGGCTAACTCTGTGC 483
Db      |||||
QY 508 CAGCAGCCGCTAATACAGAGGTCGAAGCGTTAAATCGGAATTAAGTGGGCTTAAAGCGA 567
Db      |||||
QY 484 CAGCAGCCGCTAATACAGAGGTCGAGCGTTAATCGGAATTAAGTGGGCTTAAAGCGC 543
Db      |||||
QY 568 GCGTAGGTGGCTGTGATAGTCAGATGTGAAATCCCGGCTTAACTGGGAATCTGCATCT 627
Db      |||||
QY 544 GCGTAGGTGGCTGTGATAGTCAGATGTGAGAGGTCGAGGTAATTTCTGTGTAGCGGTGAAATG 603
Db      |||||
QY 628 GAAACTGTTAGCTAGTAGGTGAGAGGTAAGTAAATTTTTCAGGTGTAGCGGTGAAATG 687
Db      |||||
QY 604 AAACTGACAGCTAGAGTATGTTAGAGGTCGAGGTAATTTCTGTGTAGCGGTGAAATG 663
Db      |||||
QY 688 CGTAGAGATCTGAAGGAATACCGATGCGAAGGACGCTTCTTCGTCATCATACTGACACTG 747
Db      |||||
QY 564 CGTAGATATAGGAAGGAACACCACTGCGGAAGGCGACCACTGGCACTGATGACACTG 723
Db      |||||
QY 748 AGGCTCGAAAGCGTGGGTAGCAAAACAGGATTTAGATACCTTCGTTAGTCCACGCGGTAAACG 807
Db      |||||
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QY 1108 CCTTAGTTACAGCAC-ITTCGGGTGGGAACTCTAAGGATATGTCACAGTGAACAACTGGAG 1166  
 DB 1084 CCTTAGTTACAGCACGTAATGGTGGGCACTCTAAGGAGACTGCGGTGACAAACCGGAG 1143  
 QY 1167 GAAGCGGGGACAGCTCAAGTCATCATGCGCCCTTACGACAGGCTACACAGTGTCTAC 1226  
 DB 1144 GAAGGTGGGGATGAGCTCAAGTCATCATGCGCCCTTACGCGCTGCGGTACACAGTGTCTAC 1203  
 QY 1227 AATGTTAGTACAGAGGGCAGCTACACAGCGATGTGATCGGAATCTCAAAAAGCCATCTCG 1286  
 DB 1204 AATGTTAGTACAGAGGGTTCAGAGCGCGAGGTGGAGCTAATCCACAAACCGATCG 1263  
 QY 1287 TAGTCAGATTTGGAGTCTGCAACTGCACTCCATGAGTAGAGTAATCGCTAGTAATCGCGGA 1346  
 DB 1264 TAGTCGGATCGAGTCTGCAACTGCACTCGCTGGAAGTCGGAATCGCTAGTAATCGCGAA 1323  
 QY 1347 TCAGAAATGCGGGGTGAATACCTTCCCGGGCTTGTACACAGCGCGCTCACACCATGGG 1406  
 DB 1324 TCAGAAATGTCGGGGTGAATACCTTCCCGGGCTTGTACACAGCGCGCTCACACCATGGG 1383  
 QY 1407 AGTTGATTTGCACAGAGGTGGTTAGCTTAA-CTTAGTGAGGGCGATCACACGGTGTGT 1465  
 DB 1384 AGTGGTTGCACAGAGTAGTAGTCTTAACCTTCGGGAGGACGTTACACAGCTGTGAT 1443  
 QY 1466 CGATGACTGGGTGAAGTCGTAAAGAGTAGCGGTAGGGGAACCTGCGCTGGATCAC 1523  
 DB 1444 TCATGACTGGGTGAAGTCGTAAAGAGTAGCGGTAGGGGAACCTGCGCTGGATCAC 1501

RESULT 5  
 US-09-793-920A-1  
 ; Sequence 1, Application US/09793920A  
 ; Patent No. US20020065389A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Canon Inc.  
 ; TITLE OF INVENTION: Polyhydroxyalkanoate containing 3-hydroxythienylalkanoic acid as  
 ; FILE OF INVENTION: monomer unit, and method for producing the same.  
 ; FILE REFERENCE: 4396021  
 ; CURRENT APPLICATION NUMBER: US/09/793,920A  
 ; CURRENT FILING DATE: 2001-02-28  
 ; NUMBER OF SEQ ID NOS: 1  
 ; SEQ ID NO 1  
 ; LENGTH: 1501  
 ; TYPE: DNA  
 ; ORGANISM: Pseudomonas jessenii 161 strain.  
 US-09-793-920A-1

Query Match 72.0%; Score 1098.6; DB 9; Length 1501;  
 Best Local Similarity 85.9%; Pred. No. 1.2e-288;  
 Matches 1287; Conservative 0; Mismatches 202; Indels 9; Gaps 6;

QY 30 GCGCGAGGCTTAACACATGCAAGTCGAGCGGAAACGATGATGCTTCTATTAGCGCTC 89  
 DB 9 GCGCGAGGCTTAACACATGCAAGTCGAGCGG--ATGACGGAGCTTGTCTCTGAATTCA 66  
 QY 90 GAGCNCGGGACGGGTGAGTAACTATTAGGAATCTACCTAGTAGTGGGGGATGATCGGG 149  
 DB 67 G---CGGCGAGGGTGAATGCTTAGGAATCTGCTGTGTAGTGGGGGACAGCTCTC 123  
 QY 150 GAACTCGAATTAATACCGCATACCT-CTACGGGAGAAAGCAGGGGNTCTATTAGACCTTG 208  
 DB 124 GAAAGGAGCGCTTAATACCGCATACCTCTCTACGGGAGAAAGCAGGGGACCTTCGGGCTTG 183  
 QY 209 CGCTATTAGATGAGCTTAAGTCGGAATAGTAGTGGGTGAAGGCTAACGCTACCATGGG 268  
 DB 184 CGCTATTAGATGAGCTTAAGTCGGAATAGTAGTGGGTGAAGGCTAACGCTACCATGGG 243  
 QY 269 ACGATCTGTAGTGTCTGAGAGGATGATCAGCCACCGGAGCTGAGACAGCGGCGGA 328  
 DB 244 ACGATCCGTAACTGTCTGAGAGGATGATCAGTCACTGGAACCTGAGACAGCGTCCAGA 303  
 QY 329 CT-CTACGGGAGGACGAGTGGGGAATTTGGACAATCGNGGGAACCTCGATCCAGCAT 387

DB 304 CTCCTACGGGAGCAGCAGTGGGGAATATTGGACAATGGCGAAAGCCTGATCCAGCCAT 363  
 QY 388 GCGCGTGTGTGAAGAGCGCTTTTGGTGTAAAGCACTTTAAAGCAGTGAAGAAGACTCT 447  
 DB 364 GCGCGTGTGTGAAGAGGCTCTTGGATTTGAAGCACTTTTAAGTTGGAGGAAGGGAT 423  
 QY 448 TCGGTTAATACCCGGGGACGATGACATTAGCTGCAGAAATAAGCACCGGCTAATCTGTGTC 507  
 DB 424 TAACTTAATACGTTAGTGTGAGCTTACCGACAGAAATAAGCACCGGCTAATCTGTGTC 483  
 QY 508 CAGCAGCGCGGTAAATACAGAGGTGCAAGCGTTAATCGGAATTAATCGGAAATTAATCGG 567  
 DB 484 CAGCAGCGCGGTAAATACAGAGGTGCAAGCGTTAATCGGAAATTAATCGGAAATTAATCGG 543  
 QY 568 CGTAGTGTGCTTGATAAGTCAGATGTGAAATCCCGGGCTTAACTCGGAACTGCATCT 627  
 DB 544 CGTAGTGTGCTTGTAAAGTTGGATGTGAAGCCCGGGCTCAACTCGGAACTGCATCT 603  
 QY 628 GAACTGTTAGGCTAGAGTAGGTAGGAGGGAAGTAGAATTTTCAAGGTGAGCGGTGAATG 687  
 DB 604 AAACTGACAAGCTAGAGTATGGTAGAGGGTGGTGAATTTTCTGTGTAGCGGTGAATG 663  
 QY 688 CGTAGAGTCTGAAGGAATACCGATGGGGAAGGAGCTTCTTGGCATCATACTGACACTG 747  
 DB 664 CGTAGATATAGGAAGGAACACCGTGGCGAAGGCGACCACTGGACTGATATCTGACACTG 723  
 QY 748 AGGCTCGAAAGCGTGGGTAGCAAAACAGGATTAGATACCTGTAGTGCACCGCGTAAACG 807  
 DB 724 AGGTGGAAGCGTGGGGAGCAACAGGATTAGATACCTGTAGTGCACCGCGTAAACG 783  
 QY 808 ATGTCTACTAGTGTGGTCCCTTGGAGCACTTAGTGACGCGAGCTTAACGCAATAGTAGA 867  
 DB 784 ATGTCAACTAGTGTGGGAGCTTTAGCTCTTAGTGGCGAGCTTAACGCAATAGTAGA 843  
 QY 868 CCGCTGGGAGTAGCGCGCAAGGTTAAACTCAATGAATTTGACGGGGGCGCCACAA 927  
 DB 844 CCGCTGGGAGTAGCGCGCAAGGTTAAACTCAATGAATTTGACGGGGGCGCCACAA 903  
 QY 928 CCGGTGGAGCATGTGTTTAAATTCGATGCAACGCGAAGCACTTACCTGCTTTCGACATA 987  
 DB 904 CCGGTGGAGCATGTGTTTAAATTCGAGCAACGCGAAGCACTTACCGAGGCTTGGACATC 963  
 QY 988 CACAGAATCTTTGATAGATACGAGAGTGCCTTCGGGAATTTGTGATACAGGTGCTGCTAG 1047  
 DB 964 CAATGAATCTTTCAGAGATGATGGTGGCTTTCGGGAACATTTGAGACAGGTGCTGCTAG 1023  
 QY 1048 CTGTCTGCTAGTCTGTGATGATGTTGGTAAAGTCCCGCAACGAGCGCAACCTTGT 1107  
 DB 1024 CTGTCTGCTAGTCTGTGATGATGTTGGTAAAGTCCCGTAAACGAGCGCAACCTTGT 1083  
 QY 1108 CTTAGTTTACCGACAC-ITTCGGGTGGGAACCTTAAGGATCTGCGAGTGACAAACTGGAG 1166  
 DB 1084 CTTAGTTTACCGACACGTAATGTGGGCACTTAAAGGAGACTGCGGTGACAAACCGGAG 1143  
 QY 1167 GAAGCGGGGACGAGCTCAAGTCAATGCGCCCTTACGACCAAGGCTACACAGTGTCTAC 1226  
 DB 1144 GAAGGTGGGATGAGCTCAAGTCAATGCGCCCTTACGCGCTGAGCTACACAGTGTCTAC 1203  
 QY 1227 AATGTTAGTACAGAGGCGAGCTACACAGCGATGTGATCGGAATCTCAAAAGGCTATCG 1286  
 DB 1204 AATGTTAGTACAGAGGCTTGCAGAGCGGAGGTGGAGCTTAATCCCAACAAACCGGATCG 1263  
 QY 1287 TAGTCCAGATTTGAGTCTGCAACTCGACTCCATCAAGTGAAGTAATCGGTAGTAATCGGGA 1346  
 DB 1264 TAGTCCGATCGAGTCTGCAACTCGACTCCGTAAGTTCGGAATCGCTAGTAATCGGGA 1323  
 QY 1347 TCAGAATGCCCGGTGAATACGTTCCCGGGCTTGTACACACCGCGCTCACACCATGGG 1406  
 DB 1324 TCAGAATGCCCGGTGAATACGTTCCCGGGCTTGTACACACCGCGCTCACACCATGGG 1383  
 QY 1407 AGTTGATTTGACAGAGTGTGTTAGCTTAA-CTTAGTGAGGCGGATCAACAGCGTGTGT 1465  
 DB 1384 AGTGGTTGACAGAGTGTGTTAGCTTAACTTTCGGGAGGACGTTACCGCGGTGTGT 1443



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; FILE REFERENCE: 4396021
; CURRENT APPLICATION NUMBER: US/09/791,610
; CURRENT FILING DATE: 2002-09-30
; NUMBER OF SEQ ID NOS: 1
; SEQ ID NO 1
; LENGTH: 1501
; TYPE: DNA
; ORGANISM: Pseudomonas jessenii 161 strain.
US-09-791-610-1

Query Match      72.0%; Score 1098.6; DB 10; Length 1501;
Best Local Similarity 85.9%; Pred. No. 1.2e-288;
Matches 1287; Conservative 0; Mismatches 202; Indels 9; Gaps 6;

QY 30 GCGCGCAGGCTTAAACACATGCAAGTCGAGCGGAAACGATGATGCTTGTCTATTAGCGCTC 89
DB 9 GCGCGCAGGCTTAAACACATGCAAGTCGAGCGG--ATGACGGGAGCTTGTCTCTGAATTCA 66
QY 90 GAGCNGCCGACGGGTGAGTAATACTTAGGAATCTACCTAGTGTAGTGGGGGATAGTCTCGGG 149
DB 67 G---CGGCGGACGGGTGAGTAATACTTAGGAATCTGCTGTGTAGTGGGGGCAACGCTCTC 123
QY 150 GAAACTCGAATTAATACCCGATACCT-CTACGGGAGAAAGCAGGGGNTCATTAGACCTTG 208
DB 124 GAAAGGACGCTAATACCGCATACCTCTTACGGGAGAAAGCAGGGGACCTTTCGGGCTTG 183
QY 209 CCCTATTAGATGAGCCTAAGTCGGATTAGCTAGATGGTGGGTAAGGCTTACCATGCG 268
DB 184 CGCTATCAGATGAGCCTAGTTCGGATTAGCTAGTGGTGGGTAAGGCTTACCATGCG 243
QY 269 AGCATCTGTAGTGTCTGAGAGGATGATCAGCCACACCGGAGCTGAGACACGCGTCCAGA 328
DB 244 AGCATCCGTAACTGTCTGAGAGGATGATCAGTCACATCGGAATGAGACACGCGTCCAGA 303
QY 329 CT-CTACGGGAGGACGAGTGGGGAATATTGGAATGNGGGAACCTGTATCGAGCAT 387
DB 304 CTCCTACGGGAGGACGAGTGGGGAATATTGGAATGNGGGAACCTGTATCGAGCAT 363
QY 388 GCGCGGTGTGAAGAGGCTTTTGGTTGTAAAGCACTTTAAAGCAGTGAAGAAGACTCT 447
DB 364 GCGCGGTGTGAAGAGGCTTTTGGTTGTAAAGCACTTTAAAGCAGTGAAGAAGGCGAT 423
QY 448 TCGGTTAATACCCGGGACGATGACATTAAGTGTGAGAAATAAGCACCGGCTAACTCTGTGC 507
DB 424 TAACTTAATACGTTAGTGTGTTTACGAGTGTACGACAGAAATAAGCACCGGCTAACTCTGTGC 483
QY 508 CAGCAGCCCGGTAATACAGAGGTGCAAGGTTAATCGGAATTAAGTGTGAGGCGTAAAGCGA 567
DB 484 CAGCAGCCCGGTAATACAGAGGTGCAAGGTTAATCGGAATTAAGTGTGAGGCGTAAAGCGC 543
QY 568 GCGTAGGTGGCTTGATAAGTCAGATGTGAAATCCCGGGCTTAACTCGGGAACCTGCACTCT 627
DB 544 GCGTAGGTGGCTTGATAAGTCAGATGTGAAATCCCGGGCTTAACTCGGGAACCTGCACTCT 603
QY 628 GAACTGTAGCTAGTGTGAGAGGAGTGAATTTTCAAGTGTAGCGGTGAATG 687
DB 604 AAACTGCAAGCTAGATGTGAGAGGTTGGAATTTTCAAGTGTAGCGGTGAATG 663
QY 688 CGTAGATCTGAAGGAATACCGATGGCGAAGGAGCTTCTGGCATCATACTGACACTG 747
DB 664 CGTAGATCTGAAGGAATACCGATGGCGAAGGAGCTTCTGGCATCATACTGACACTG 723
QY 748 AGGCTCGAAGGCTGGGTAGCAAAACAGGATTAGATACCTGTAGTCCACCGGTAACG 807
DB 724 AGGCTCGAAGGCTGGGTAGCAAAACAGGATTAGATACCTGTAGTCCACCGGTAACG 783
QY 808 ATGCTACTAGTCTGTGGGTCCCTTTAGGACTTAGTGACGAGCTTAACGCAATTAAGTGA 867
DB 784 ATGCTCACTAGCGTTGGAGCTTTGAGCTCTTAGTGGCGAGCTTAACGCAATTAAGTGA 843
QY 868 CCGCTCGGGAGTACGGCGCAAGGTTAAACTCAAATGAATTAAGCGGGGCGCGCAAA 927
DB 844 CCGCTCGGGAGTACGGCGCAAGGTTAAACTCAAATGAATTAAGCGGGGCGCGCAAA 903
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QY 928 GCGGTGGAGCATGTGGTTTAAATTCGATGCAACGCGAAGAACTTACCTGGTCTTGCACATA 987
DB 904 GCGGTGGAGCATGTGGTTTAAATTCGAGCAACGCGAAGAACTTACCGAGGCTTGCACATC 963
QY 988 CACAGAAATCTTTAGAGATACGAGAGTGCCCTTCGGGAAATTGTGATACAGGTGCTCATGG 1047
DB 964 CAATGAACTTTCCAGAGATGATGGGTGCCCTTCGGGAAACATTTAGACAGGTGCTCATGG 1023
QY 1048 CTGTGCTGAGCTGTGCTGAGATGTTGGGTTAAGTCCCGCAAGGAGCGCAACCTTGT 1107
DB 1024 CTGTGCTGAGCTGTGCTGAGATGTTGGGTTAAGTCCCGTAACGAGCGCAACCTTGT 1083
QY 1108 CCTTAGTTTACCAGCAC--TTCCGGGTGGGAACTCTTAAGGATCTGCGCAGTGACAAACTGAG 1166
DB 1084 CCTTAGTTTACCAGCACCGTAATGGTGGGCACTCTTAAGGAGACTGCGGTGACAAACCGGAG 1143
QY 1167 GAAGCGGGGACGACGTCATCATATGCGCCCTTACGACAGGCTTACACAGGTGCTAC 1226
DB 1144 GAAGTGGGGATGACGTCAGTCAAGTCAATGCGCCCTTACGCGCTGGGCTACACACGCTGCTAC 1203
QY 1227 AATGTTAGGTACAGAGGCGACCTACACAGCGATGTGATGCGAATCTCAAAAGCCTATCG 1286
DB 1204 AATGTTAGGTACAGAGGCTTCCCAAGCGCGAGGTGGAGCTAATCCCAAAACCGGATCG 1263
QY 1287 TAGTCCAGATTGGAGTCTGCAACTCGACTCCATGAAGTAGGAATCGCTAGTAATCGCGGA 1346
DB 1264 TAGTCCGAGTCGCACTCTGCAACTCGACTCGTGAAGTTCGGAATCGCTAGTAATCGCGGA 1323
QY 1347 TCAGAAATGCCCGGTGAATACGTTCCCGGGCTTTGTACACACGCGCTTACACCATGG 1406
DB 1324 TCAGAAATGTCGCGGTGAATACGTTCCCGGGCTTTGTACACACGCGCTTACACCATGG 1383
QY 1407 AGTTGATTGACACAGAGTGGTTAGCCTAA--CTTAGTGAGGCGCATCACCGGTGCTGAT 1465
DB 1384 AGTGGGTGACACAGAGTGGTTAGCCTAA--CTTAGTGAGGAGACGCTTACCGGTGCTGAT 1443
QY 1466 CGATTGACTGGGCTGAAAGTCGTAACAGGTAGCCCTAGGGGAACTTGGCGCTGGATCAC 1523
DB 1444 TCATGACTGGGCTGAAAGTCGTAACAGGTAGCCCTAGGGGAACTTGGCGCTGGATCAC 1501
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RESULT 8

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US-10-218-519-5
; Sequence 5, Application US/10218519
; Publication No. US20030049806A1
; GENERAL INFORMATION:
; APPLICANT: Yano, Tetsuya
; APPLICANT: Imamura, Takeshi
; APPLICANT: Suda, Sakae
; APPLICANT: Honma, Teutomu
; TITLE OF INVENTION: Polyhydroxyalkanoate Synthase and Gene Encoding the Same Enzyme
; FILE REFERENCE: 03500.015225.1
; CURRENT APPLICATION NUMBER: US/10/218,519
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/821,016
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Microsoft Word
; SEQ ID NO 5
; LENGTH: 1501
; TYPE: DNA
; ORGANISM: Pseudomonas jessenii P161 ; BP-7376
; FEATURE:
; FEATURE: cdna to 16S rRNA
US-10-218-519-5
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Query Match      72.0%; Score 1098.6; DB 14; Length 1501;
Best Local Similarity 85.9%; Pred. No. 1.2e-288;
Matches 1287; Conservative 0; Mismatches 202; Indels 9; Gaps 6;

QY 30 GCGCGCAGGCTTAAACACATGCAAGTCGAGCGGAAACGATGATGCTTGTCTATTAGCGCTC 89
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Db 9 GGGCGGAGGCTAACACATGCAAGTCGAGCGG--ATGACGGGAGCTTGCTCCTGAATTCA 66  
Qy 90 GAGNCCGAGCGGTGAGTAATCTAGTAATCTACCTAGTAGTGGGGATAGTCTCGG 149  
Db 67 G---CGCGGAGCGGTGAGTAATGCTTGAAGTAATGCTGTTGAGGAGCAACGCTC 123  
Qy 150 GAAACTCGAATTAATACCGCATAGCT-CTACGGGAGAAAGCAGGGGNTCAATTAGACTTG 208  
Db 124 GAAAGGACGCTAATACCGCATAGCTCTACGGGAGAAAGCAGGGGACTTTCGGGCTTG 183  
Qy 209 CGCTATTAGATGACCTTAAGTCGGAATTAGTGGGTAAAGCCCTACATGGCG 268  
Db 184 CGCTATCAGATGACCTTAGTTCGGAATTAGTGGGTAAAGCCCTACATGGCG 243  
Qy 269 ACGATCTGTAGTCTGTAGAGGATGATCAGCCACACCGGGACTGAGACCGGCCCGGA 328  
Db 244 ACGATCCGTAACCTGTGTAGAGGATGATCAGTCACACTGGAATGAGACACCGTCCGA 303  
Qy 329 CT-CTACGGGAGGAGCAGTGGGGAATTTGGACAATGNGGGAACCCCTGATCCAGGCAT 387  
Db 304 CTCTACGGGAGGAGCAGTGGGGAATTTGGACAATGNGGGAACCCCTGATCCAGGCAT 363  
Qy 388 GCGCGTGTGTGAAGAAGGCTTTTGGTTGTAAAGCACTTTAAGCAGTGAAGAAGACTCT 447  
Db 364 GCGCGTGTGTGAAGAAGGCTTTTGGATTGTAAAGCACTTTAAGTTGGGAGGAAGGCAT 423  
Qy 448 TCGGTTAATACCGGGAGACATGACATTTAGCTGCAGTAATAGCACCGGCTAACTCTGTGC 507  
Db 424 TAACCTAATACGTTAGTGTGTTGACGTTTACCGACAGAAATAGCACCGGCTAACTCTGTGC 483  
Qy 508 CAGCAGCGCGGTAAATACAGAGGTCGAAGCGTTTAATCGGAATTTACTGGGCGTAAAGCGA 567  
Db 484 CAGCAGCGCGGTAAATACAGAGGTCGAAGCGTTTAATCGGAATTTACTGGGCGTAAAGCGC 543  
Qy 568 GCGTAGTGGCTTGATTAAGTCAAGTGTGAATATCCCGGGCTTAACCTGGGAATGCAATCT 627  
Db 544 GCGTAGTGGCTTGATTAAGTGTGAATATCCCGGGCTTAACCTGGGAATGCAATCT 603  
Qy 628 GAACTCTTAGGCTAGTAGTGTGAGGGAAGTGTAGAAATTTCAAGTGTAGCGGTGAATG 687  
Db 604 AAAACTCACAAGCTAGTAGTGTGAGGGAAGTGTAGAAATTTCTGTGTAGCGGTGAATG 663  
Qy 688 CGTAGAGATCTGAAGGAATACCGATGCGAAGGAGCTTCTTGGCATCATACTGACACTG 747  
Db 664 CGTAGATATAGGAAGGAACACCACTGCGGAAGGCGACCACTGGAATGATGACACTG 723  
Qy 748 AGGCTCGAAAGCGGTGTAGCAAAACAGATTTAGATACCTGTGTAGTCCACCGCGTAAAG 807  
Db 724 AGGTGCGAAAGCGGTGTAGCAAAACAGATTTAGATACCTGTGTAGTCCACCGCGTAAAG 783  
Qy 808 ATGTCTACTAGTCTGTGGTCCCTTGGAGACTTAGTCAGCAGCTAACGCAATAAGTAGA 867  
Db 784 ATGTCAACTAGCTGTGGAGCCTTGTAGCTCTTAGTGCGGAGCTTAACGATTAAGTTGA 843  
Qy 868 CCGCTCGGGAGTAGCGGCGCAAGGTTAAATCGAATTTGACGGGGCGCGCACAA 927  
Db 844 CCGCTCGGGAGTAGCGGCGCAAGGTTAAATCGAATTTGACGGGGCGCGCACAA 903  
Qy 928 GCGGTGAGCATGTGTTTAAATTCGATGCAACGGGAAGAACCTTACCTGTCTTGACATA 987  
Db 904 GCGGTGAGCATGTGTTTAAATTCGAAAGCAACGGGAAGAACCTTACCAGGCTTTGACATC 963  
Qy 988 CACAGAACTTTGTAGAGATACGAGTGCCTTTCGGGAATTTGTATACAGTGTGTCATGG 1047  
Db 964 CAATGAATCTTCCAGAGATGATGGGTGCCTTTCGGGAACATTTGAGACAGGTGTGCAATG 1023  
Qy 1048 CTGTCTGTCAGCTCGTGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCCTGT 1107  
Db 1024 CTGTCTGTCAGCTCGTGTGAGATGTTGGGTTAAGTCCCGTAAAGCGCAACCCCTGT 1083  
Qy 1108 CTTAGTTACAGAC--TTCCGGGTGGGAATCTTAAGGATGATGCGAGTGAACAACTGGAG 1166  
Db 1084 CTTAGTTACAGACCGTAATGGTGGGCACTCTAAGGAGACTTCCCGGTGAACAAACCGGAG 1143

RESULT 9

US-10-266-787-5  
; Sequence 5, Application US/10286787  
; Publication No. US2003008277A1  
; GENERAL INFORMATION:  
; APPLICANT: Yano, Tetsuya  
; APPLICANT: Imamura, Takeshi  
; APPLICANT: Suda, Sakae  
; APPLICANT: Honma, Tsutomu  
; TITLE OF INVENTION: Polyhydroxyalkanoate Synthase and Gene Encoding the Same Enzyme  
; FILE REFERENCE: 03500.015225.3  
; CURRENT APPLICATION NUMBER: US/10/266,787  
; CURRENT FILING DATE: 2002-10-09  
; PRIOR APPLICATION NUMBER: JP 2000-095004  
; PRIOR FILING DATE: 2000-03-30  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: Microsoft Word  
; SEQ ID NO 5  
; LENGTH: 1501  
; TYPE: DNA  
; ORGANISM: Pseudomonas jessenii Pj61 ; BP-7376  
; FEATURE:  
; FEATURE: cDNA to 16S rRNA  
US-10-266-787-5

Query Match 72.0%; Score 1098.6; DB 14; Length 1501;  
Best Local Similarity 85.9%; Pred.No. 1.2e-288;  
Matches 1287; Conservative 0; Mismatches 202; Indels 9; Gaps 6;  
Qy 30 GCGCGCAGGCTTAACACATGCAAGTCGAGCGGAAACGATAGCTGTGCTTAATGAGCGTC 89  
Db 9 GCGCGCAGGCTTAACACATGCAAGTCGAGCGG--ATGACGGGAGCTTGTCTCTGAATTCA 66  
Qy 90 GAGCNGCCGAGCGGTGAGTAATCTAGTAATCTACCTAGTAGTGGGGATAGTCTCGG 149  
Db 67 G---CGCGGAGCGGTGAGTAATGCTTGAAGTAATGCTGTTGAGTGGGAGCAACGCTC 123  
Qy 150 GAACTCGAATTAATACCGCATAGCT-CTACGGGAGAAAGCAGGGGNTCAATTAGACTTG 208  
Db 124 GAAAGGACGCTAATACCGCATAGCTCTACGGGAGAAAGCAGGGGACTTTCGGGCTTG 183  
Qy 209 CGCTATTAGATGACCTTAAGTCGGAATTAGTGGGTAAAGCCCTACATGGCG 268  
Db 184 CGCTATCAGATGACCTTAGTTCGGAATTAGTGGGTAAAGCCCTACATGGCG 243  
Qy 269 ACGATCTGTAGTCTGTAGAGGATGATCAGCCACACCGGGACTGAGACCGGCCCGGA 328

Db 244 ACGATCCGTAACGTGCTGAGAGGATGATCACTGCACTGGAACCTGAGACACGGTCCAGA 303  
QY 329 CT-CTACGGAGGACAGCAGTGGGGAATATTGGACAATGGNGGAACCCCTGATCCAGCCAT 387  
Db 304 CTCCTACGGAGGACAGCAGTGGGGAATATTGGACAATGGGCGAAGCCCTGATCCAGCCAT 363  
QY 388 GCCCGGTGTGTGAAGAAGCCCTTTTGGTGTAAAGCACATTTAAAGCAGTGAAGAAGACTCT 447  
Db 364 GCCCGGTGTGTGAAGAAGCTTTCGGATTGTAAAGCACATTTAAAGTGGGAGGAGGCAT 423  
QY 448 TCGGTTAATACCCGGGCGAGTACATTAAGTGCAGAAATAGCACCGGCTAACTCTGTGC 507  
Db 424 TAACTAATACCTTGTAGTGTGGTACCGGCTAACACAGAAATAGCACCGGCTAACTCTGTGC 483  
QY 508 CAGCAGCCGCGTAATACAGAGGCTGCAAGCGTAAATCGGAATTAATCTGGGCGTAAAGCGA 567  
Db 484 CAGCAGCCGCGTAATACAGAGGCTGCAAGCGTAAATCGGAATTAATCTGGGCGTAAAGCGC 543  
QY 568 GCGTAGGTGGCTGATTAAGTACAGTGTGAAATCCCGGGCTTAACTCTGGGAACTGCATCT 627  
Db 544 GCGTAGGTGGTGTGTTAGTGTGATGTGAAAGCCCGGCTCAACTGGGAACCTGCATTC 603  
QY 628 GAAACTGTAGCTAGTGTAGAGGAGTGAAGTAACTTCCAGTGTAGCGGTGAATG 687  
Db 604 AAACTGCAACAGCTAGATGTAGAGGCTGTGGAATTTCTGTGTAGCGGTGAATG 663  
QY 688 CGTAGAGATCTGAAGGAATACCGATGGCGAAGCGAGCTTCTTGGCATCATACTGACATG 747  
Db 664 CGTAGATATAGGAAGGAACACAGTGGCGAAGCGACCACTGGACTGATCTGACATG 723  
QY 748 AGGCTGGAAGCGTGGGTAGCAAAACAGGATTAAGTACCTGTGTAGTCCAGCGGTAACG 807  
Db 724 AGGTGCAAAAGCGTGGGAGCAACAGGATTAAGTACCTGTGTAGTCCAGCGGTAACG 783  
QY 808 ATGTCTACTAGTCTGGTCCCTTGGAGCTTGTAGTACGAGCTTAAAGCAATAGTAGA 867  
Db 784 ATGTCAACTAGCTGTGGGAGCTTGTAGTGTGGGAGCTTAAAGCAATAGTAGA 843  
QY 868 CGGCTCGGGAGTACGGCGCAAGGTAAAGCTCAAACTGAAATGACGGGGCGGCACAA 927  
Db 844 CGGCTCGGGAGTACGGCGCAAGGTAAAGCTCAAACTGAAATGACGGGGCGGCACAA 903  
QY 928 GCGGTGGAGCATGTGGTAAATTCGATGCAACGCAAGAACCTTACCTGGTCTTGACATA 987  
Db 904 GCGGTGGAGCATGTGGTAAATTCGATGCAACGCAAGAACCTTACCTGGTCTTGACATC 963  
QY 988 CACAGAACTTGTAGAGATACAGAGTGGCTTCGGGAATTTGATACAGGTGCTGCATGG 1047  
Db 964 CAATGAACCTTCCAGAGATGGATGGGTGCTTTCGGGAACTTTGAGACAGGTGCTGCATGG 1023  
QY 1048 CTGTCTCAGCTCGTGTGTGAGATGTTGGGTAAAGTCCCGCAACGAGCGCAACCTTGT 1107  
Db 1024 CTGTCTCAGCTCGTGTGTGAGATGTTGGGTAAAGTCCCGTAAAGCGGCAACCTTGT 1083  
QY 1108 CTTTGTAGTTACCAAGC-CTTCGGGTGGGAACCTTAAAGTACTTCCAGTGCAGCAAACTGGAG 1166  
Db 1084 CTTTGTAGTTACCAAGCAGTAAATGTTGGGCACCTTAAAGGAGACTTCCGGGTGACAAACCGGAG 1143  
QY 1167 GAAGCGGGGACGCTCAAGTCAATGCGCCCTTACGACAGGCTACACAGGTGCTAC 1226  
Db 1144 GAAGCGGGGATGACGCTCAAGTCAATGCGCCCTTACGCGCTTACGCGCTGCTAC 1203  
QY 1227 AATGTTAGTACAGAGGCGAGTACACAGCGATGTGATCGGAATCTCAAAAGCCATCG 1286  
Db 1204 AATGTTAGTACAGAGGCTTCCAGCGCGGAGGTGGAGCTAATCCCAAAACCGATCG 1263  
QY 1287 TAGTCCAGATGGAGTCTGCAACTCGACTTCCAGTGAAGTAGGAATCGCTAGTAATCGCGGA 1346  
Db 1264 TAGTCCGATCGAGTCTGCAACTCGACTGCGTGAAGTCGGAATCGCTAGTAATCGCGGA 1323  
QY 1347 TCAGAAATCCCGGCTGAATACGTTCCCGGCTTGTACACACCGGCTGACACCATGG 1406  
Db 1324 TCAGAAATCGCGGCTGAATACGTTCCCGGCTTGTACACACCGGCTGACACCATGG 1383

QY 1407 AGTTGATTGCCAGGAAGTGGTTAGCCTAA-CTTAGTGAGGCGGATCACCACGGTGTGGT 1465  
Db 1384 AGTGGTTGCCACGAGAGTAGTCTAGCTTAACTTCCGGAGGACGGTTACCACGGTGTGAT 1443  
QY 1466 CGATGACTGGGGTGAAGTCTGTAAACAAGTAGCCGTAGGGAACTTCGGGTGGATCAC 1523  
Db 1444 TCATGACTGGGGTGAAGTCTGTAAACAAGTAGCCGTAGGGAACTTCGGGTGGATCAC 1501  
RESULT 10  
US-10-252-518-5  
; Sequence 5, Application US/10252518  
; Publication No. US20030087413A1  
; GENERAL INFORMATION:  
; APPLICANT: Yano, Tetsuya  
; APPLICANT: Imamura, Takeshi  
; APPLICANT: Suda, Sakae  
; APPLICANT: Honma, Tsutomu  
; TITLE OF INVENTION: Polyhydroxyalkanoate Synthase and Gene Encoding the Same Enzyme  
; FILE REFERENCE: 03500.015225.2  
; CURRENT APPLICATION NUMBER: US/10/252,518  
; CURRENT FILING DATE: 2002-09-24  
; PRIOR APPLICATION NUMBER: JP 2000-095004  
; PRIOR FILING DATE: 2000-03-30  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: Microsoft Word  
; SEQ ID NO 5  
; LENGTH: 1501  
; TYPE: DNA  
; ORGANISM: Pseudomonas jessenii P161 ; BP-7376  
; FEATURE:  
; FEATURE: cDNA to 16S rRNA  
US-10-252-518-5  
Query Match 72.0%; Score 1098.6; DB 14; Length 1501;  
Best Local Similarity 85.9%; Pred. No. 1.2e-288;  
Matches 1287; Conservative 0; Mismatches 202; Indels 9; Gaps 6;  
QY 30 GCGCGCAGGCTTAACACATGCAAGTCGAGCGGAACGATAGTCTCTATTAGGCGTC 89  
Db 9 GCGCGCAGGCTTAACACATGCAAGTCGAGCGG--ATGACGGGAGCTTCTCTGAAATCA 66  
QY 90 GAGCNGCGGACGGGTGAGTAATCTTAGGAATCTACCTAGTAGTGGGGGATAGTCGGG 149  
Db 67 G---CGCGGACGGGTGAGTAATCGCTAGGAATCTGCTGTGTAGTGGGGGACAGCTC 123  
QY 150 GAAACTCGAATTAATACCGCATACGT-CTACGGGAGAAAGCAGGGGNTCATTTAGACCTTG 208  
Db 124 GAAAGGAGCGCTAATACCGCATACGTCTACGGGAGAAAGCAGGGGACCTTCGGGCTTG 183  
QY 209 CGCTATTAGATGCGCTAAGTCGGATAGCTAGATGGTGGGTAAGGCTTACCATGGG 268  
Db 184 CGCTATCAGATGAGCCCTAGGTAGCTAGTGTGGTGGTAAAGCTTACCAAGCGG 243  
QY 269 ACATCTGTAGCTGTGAGAGGATGATCAGCACACCGGAGCTGAGACACGGCCCGGA 328  
Db 244 ACATCGGTAACTGTCTGAGAGGATGATCACTCACTGGAATCTGAGACACGGTCCAGA 303  
QY 329 CT-CTACGGGAGGACGAGTGGGGAATTTTGGACAATAGGNGGGAACCTTGATCCAGCCAT 387  
Db 304 CTCCTACGGGAGGACGAGTGGGGAATTTTGGACAATAGGNGGGAACCTTGATCCAGCCAT 363  
QY 388 GCCCGGTGTGTGAAGAAGCCCTTTTGGTGTAAAGCACTTTTAAAGCTGGAAGAGACTCT 447  
Db 364 GCCCGGTGTGTGAAGAAGGCTTTCGGATTGTAAAGCACTTTTAAAGTGGGAGGAGGCAAT 423  
QY 448 TCGGTTAATACCCGGGACCGATGACATTAAGTCTGAGAAATAGCACCGGCTAACTCTGTGC 507  
Db 424 TAACTAATACGTTAGTGTGTTTGGAGTTTACCGACAGAAATAGCACCGGCTAACTCTGTGC 483  
QY 508 CAGCAGCGCGGTAAATACAGAGGTGCAAGCGTAAATCGGAATTTACTCGGAATTTACTGGGCGTAAAGCGA 567

Db 484 CAGCAGCCGCGTAATACAGAGGTGCAAGCGTTAATCGGAATTACTTGGCGTAAAGCGC 543  
 QY 568 GCGTAGGTGGCTTGAATAGTCAAGTGTGAATATCCCGGGCTTAACCTGGGAACATGCAATCT 627  
 Db 544 GCGTAGGTGGCTTGTAAAGTTGGATGTGAAGCCCGGGCTCAACCTGGGAACATGCAATC 603  
 QY 628 GAAACTGTTAGGTAGCTAGCTAGAGAGGGAAGTAGAATTTTCAGGTGTAGCGGTGAATG 687  
 Db 604 AAACTGACAGCTAGAGTATGGTAGAGGGTGGTGAATTTTCCTGTGTAGCGGTGAATG 663  
 QY 688 CGTAGATCTGAAGGAATACCGATGGCGAAGGAGCTTCTCGGCATCATACTGACACTG 747  
 Db 664 CGTAGATATAGGAAGAACACAGTGGCGAAGGCGACCACTGGACTGATACTGACACTG 723  
 QY 748 AGGCTGAAAGCGTGGTAGCAACACAGGATTAGATACCTCTGGTGTACCGCCGTAAACG 807  
 Db 724 AGGTGCGAAAGCGTGGGAGCAACACAGGATTAGATACCTCTGGTGTACCGCCGTAAACG 783  
 QY 808 ATGTCTACTAGTCTGGTGGCTTGGAGACTTGTAGGACTTGTAGTACGAGCTTAACGCAATAGTAGA 867  
 Db 784 ATGTCAACTAGCCGTTGGAGCCTTGACTCTTATGTGGCGGAGCTTAACGCAATAGTTGA 843  
 QY 868 CGCCTGGGAGTAGCGGCCGCAAGGTTAAAACTCAAAATGAATTGACGGGGGCCCGCACAA 927  
 Db 844 CCGCTGGGAGTAGCGGCCGCAAGGTTAAAACTCAAAATGAATTGACGGGGGCCCGCACAA 903  
 QY 928 GCGGTGGAGCATGTGTTTAATTCGATGCAACGCGAAGAACTTACCTGTGCTTGAATG 987  
 Db 904 GCGGTGGAGCATGTGTTTAATTCGAAAGCAACGGAAGAACTTACCGAGGCTTGAATC 963  
 QY 988 CACGAATCTTGTAGAGATACGAGAGTGCCCTTCGGGAATTTGTATACAGGTGCTGCAATG 1047  
 Db 964 CAATGAATCTCCAGAGATGATGGTGCCCTTCGGGAACATTGAGACAGGTGCTGCAATG 1023  
 QY 1048 CTGTCGTGAGTGTGCTGAGATGTTGGTGTAAAGTCCCGCAACGAGCGCAACCTTGT 1107  
 Db 1024 CTGTCGTGAGTGTGCTGAGATGTTGGTGTAAAGTCCCGTAAAGAGGCGCAACCTTGT 1083  
 QY 1108 CCTAGTTTACCAGCAC-TTCGGGTGGGAACCTTAAGGATCTAAGGATCTCAGTGACAACTGGAG 1166  
 Db 1084 CCTAGTTTACCAGCACGAATGGTGGGCACTCTAAGGAGACTGCGCGGTGACAAACCGGAG 1143  
 QY 1167 GAAGCGGGGACGACGTCAAGTCTCATGGGCCCTTACGACGAGGCTACACAGCTGCTAC 1226  
 Db 1144 GAAGTGGGATGACGTCAAGTCTCATGGGCCCTTACGCGCTGGGCTACACAGCTGCTAC 1203  
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 Db 1204 AATGTTAGGTAACAGGCGGTTCGCAAGCGCGAGGTGGAGCTTAATCCCAAAAACCGATCG 1263  
 QY 1287 TAGTCCGATTTGGAGTCTGCAACTCGACTCCATCAAGTATGGAATCGCTAGTAAATCGCGGA 1346  
 Db 1264 TAGTCCGATTCGCAAGTCTGCAACTCGACTCGTGAAGTTCGGAATTCGCTAGTAAATCGGAA 1323  
 QY 1347 TCAGAATGCCCGGTGAATAGCTTCCCGGGCCTTGTACACACCGCCCGGTACACACCATGGG 1406  
 Db 1324 TCAGAATGTCGCGTGAATAGCTTCCCGGGCCTTGTACACACCGCCCGGTACACACCATGGG 1383  
 QY 1407 AGTTGATTCACAGAGTGTGTAGCTAA-CTTAGTAGAGGGCGGATCACACGCTGTGGT 1465  
 Db 1384 AGTGGGTTCACAGAGTGTGTAGCTAACTTTCGGGAGGACGTTTACCACGCTGTGAT 1443  
 QY 1466 CGATGACTGGGGTGAAGTCGTAACAAAGTAGCCGTAGGGAACTCGCGCTGGATCAC 1523  
 Db 1444 TCATGACTGGGGTGAAGTCGTAACAAAGTAGCCGTAGGGAACTCGCGCTGGATCAC 1501

## RESULT 11

US-10-105-305-1  
 ; Sequence 1, Application US/10105305  
 ; Publication No. US20030096182A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: CANON KABUSHIKI KAISHA

; TITLE OF INVENTION: POLYHYDROXYALKANOATE CONTAINING UNIT WITH THIENYL STRUCTURE IN THE  
 ; TITLE OF INVENTION: CHAIN, PROCESS FOR ITS PRODUCTION, CHARGE CONTROL AGENT, TONER B  
 ; TITLE OF INVENTION: TONER WHICH CONTAIN THIS POLYHYDROXYALKANOATE, AND IMAGE-FORMING  
 ; TITLE OF INVENTION: IMAGE-FORMING APPARATUS WHICH MAKE USE OF THE TONER  
 ; FILE REFERENCE: CPO16309  
 ; CURRENT APPLICATION NUMBER: US/10/105,305  
 ; CURRENT FILING DATE: 2002-03-26  
 ; PRIOR APPLICATION NUMBER: JP 2001-090026, JP 2001-133551  
 ; PRIOR FILING DATE: 2001-3-27, 2001-4-27  
 ; NUMBER OF SEQ ID NOS: 1

; SEQ ID NO 1  
 ; LENGTH: 1501  
 ; TYPE: DNA  
 ; ORGANISM: Pseudomonas jessenii 161 strain.  
 ; US-10-105-305-1

Query Match 72.0%; Score 1098.6; DB 14; Length 1501;  
 Best Local Similarity 85.9%; Pred. No. 1.2e-288;  
 Matches 1287; Conservative 0; Mismatches 202; Indels 9; Gaps 6;

QY 30 GGCGGCGAGGCTTAACACATGCAAGTCGAGCGGAAACGATAGCTTGTCTATTAGCGTC 89  
 Db 9 GGCGGCGAGGCTTAACACATGCAAGTCGAGCGG--ATGACGGGAGCTTGTCTCTGAATCA 66  
 QY 90 GAGCGCGGACGCGGTGAGTAATCTAGGAATCTACCTAGTAGTGGGGATAGCTCGGG 149  
 Db 67 G---CGCGGACCGGTGAGTAATGCTTAGGAATCTGCTGTGTAGTGGGGACAACTGTC 123  
 QY 150 GAAACTCGAATTAATACCGCATACGT-CTACGGGAGAAAGCAGGGGNNCTATTAGACCTTG 208  
 Db 124 GAAAGGAGCGCTAATACCGCATACGCTCTACGGGAGAAAGCAGGGGACCTTTCGGGCTTG 183  
 QY 209 CGCTATTAGATGACCTTAAGTCGGATTAGCTAGATGGTGGGTAAAGCCCTACCATGGCG 268  
 Db 184 CGCTATCAGATGACCTTAGTTCGGATTAGCTAGTTCGGTGAAGTAAATGGCTCACCAAGCG 243  
 QY 269 ACCATCTGAGTGTGCTGAGAGGATGATCAGCCACACCGGGACTGAGACACGCGCCCGGA 328  
 Db 244 ACCATCTGTAACCTGCTGAGAGGATGATCAGTCACTGGAACCTGAGACACCGTCCAGA 303  
 QY 329 CT-CTACGGGAGGACGAGTGGGGAATATTGGCAATATGNGGGAACCTTGAATCCAGCCAT 387  
 Db 304 CTCCTACGGGAGGACGAGTGGGGAATATTGGCAATATGNGGGAACCTTGAATCCAGCCAT 363  
 QY 388 GCGCGCTGTGTGAAGAAGCCCTTTTGGTGTAAAGCACTTTAAGCACTGAAGAGACTCT 447  
 Db 364 GCGCGCTGTGTGAAGAAGGCTTTCGGAATTGTAAAGCACTTTAAGTGTGGGAGGAAGGCGAT 423  
 QY 448 TCGGTTTAATACCCCGGAGCATGACATTAAGTTCAGAAATAAGCACCGGCTTAACCTGTGTGC 507  
 Db 424 TAACCTTAATACGTTAGTGTGTTTACCGTACCAGACAGAAATAGCACCGGCTAACTCTGTGC 483  
 QY 508 CAGCAGCCCGGTAAATACAGAGGTCGAAGCGTTAATTCGGAATTAATCTGGGCGTAAAGCGA 567  
 Db 484 CAGCAGCCCGGTAAATACAGAGGTCGAAGCGTTAATTCGGAATTAATCTGGGCGTAAAGCGC 543  
 QY 568 GCGTAGGTGCTTGAATGATGATGATGAAATCCCGGGCTTAACCTGGGAACCTGATCT 627  
 Db 544 GCGTAGGTGCTTGAATGATGATGATGAAAGCCCCGGGCTCAACCTGGGAACCTGATTC 603  
 QY 628 GAAACTGTTAGGCTAGAGTAGGTGAGAGGGAAGTAGAATTTTCAGGTGTAGCGGTGAAATG 687  
 Db 604 AAACTGACAGCTAGAGTATGTTAGAGGTGTGGGAATTTCTGTGTAGCGGTGAAATG 663  
 QY 688 CGTAGAGATCTGAAGGAATACCGATGCGGAAGGAGCTTCTCTGGCATCATCTGACACTG 747  
 Db 664 CGTAGATATAGGAAGGAACACCCAGTGGCGAAGGCGCACCTTGGACTGATCTGACACTG 723  
 QY 748 AGGCTCGAAAGCGTGGTAGCAAAAGGATTAAGATACCTCTGGTGTAGTCCACGCGTAAACG 807  
 Db 724 AGGTGCGAAAGCGTGGGAGCAACACAGGATTAAGATACCTCTGGTGTAGTCCACGCGTAAACG 783  
 QY 808 ATGTCTACTAGTCTGTTGGTCCCTTGGAGCACTTGTAGTACGAGCTTAACGCAATAGTAGA 867

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Db 784 ATGTCAACTAGCGTGTGGAGCCTTTAGCTCTTAGTGGCGAGCTAAACGCATTAAAGTTGA 843
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Db 844 CCGCTCTGGGAGTACGGCGCAAGGTTAAACCTCAAAATCAATTAAGTACGGGGCCCGCACAA 903
Qy 928 GCGGTGGAGCATGTGTTTAAATTCGATGCAACCGCAAGAACCTTACCTGGTCTTGACATA 987
Db 904 GCGGTGGAGCATGTGTTTAAATTCGATGCAACCGCAAGAACCTTACCTGGTCTTGACATC 963
Qy 988 CACAGAACTTTGTAGAGATACAGAGTGTCTTCGGGAATTGAGATACAGGTGTCTGCATGG 1047
Db 964 CAATGAACCTTTCCAGAGATGAGTGGTGTCTTCGGGAACATTTGACACAGGTGTCTGCATCG 1023
Qy 1048 CTGTGCTCAGCTCGTGTGAGATGTTGGTGTAAAGTCCGCAACGAGCGCAACCTCTGT 1107
Db 1024 CTGTGCTCAGCTCGTGTGAGATGTTGGTGTAAAGTCCGCAACGAGCGCAACCTCTGT 1083
Qy 1108 CCTTAGTTTACCAGCAC-TTTCGGGTGGGAACCTTAAGGATACCTGCGAGTGAACAACTGGAG 1166
Db 1084 CCTTAGTTTACCAGCACGTAATGTTGGGCACTCTAAGGAGACTGCGGTGACAAACCGGAG 1143
Qy 1167 GAAGCGGGGAGCAGCTCAAGTCATCATGCGCCCTTACGACAGGCTTACACAGTGTAC 1226
Db 1144 GAAGTGGGGATGAGCTCAAGTCATCATGCGCCCTTACGCGCTGGGCTACACAGTGTAC 1203
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Db 1204 AATGTCGGTACAGAGGGTTGCCAAGCCGCGAGGTGGAGCTAATCCCAACAAACCGATCG 1263
Qy 1287 TAGTCCAGATGAGCTGCAACTCGAATCGAATGAGTAAAGTAAAGTAAAGTAAAGTAAAGT 1346
Db 1264 TAGTCCGATCGCACTCTGCAACTCGAATGAGTAAAGTAAAGTAAAGTAAAGTAAAGT 1323
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Db 1324 TCAGAAATGCGCGTGAATACGTTCCCGGGCTTGTACACACCGCCCTGTCACACATGGG 1383
Qy 1407 AGTTGATGTCACCAAGTGGTTAGCTTAA-CTTAGTAGGCGGATCACCGGTGTGGT 1465
Db 1384 AGTGGTGTGACCAAGTGGTTAGCTTAA-CTTAGTAGGCGGATCACCGGTGTGGT 1443
Qy 1466 CGATGACTGGGTGAAGTCGTAACAAAGTGTAGCGGTAGGGAACCTGCGGCTGGATCAC 1523
Db 1444 TCATGACTGGGTGAAGTCGTAACAAAGTGTAGCGGTAGGGAACCTGCGGCTGGATCAC 1501
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## RESULT 12

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US-10-133-404A-1
; Sequence 1, Application US/10133404A
; Publication No. US20030104302A1
; GENERAL INFORMATION:
; APPLICANT: Tsutomu Honma
; APPLICANT: Tetsuya Yano
; APPLICANT: Tsuyoshi No. US20030104302A1oto
; APPLICANT: Shinya Kozaki
; TITLE OF INVENTION: Construct and Method for Making It
; FILE REFERENCE: CF016374
; CURRENT APPLICATION NUMBER: US/10/133,404A
; CURRENT FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: JP P2001-131694
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: JP P2001-208704
; PRIOR FILING DATE: 2001-07-10
; NUMBER OF SEQ ID NOS: 13
; SEQ ID NO 1
; LENGTH: 1501
; TYPE: DNA
; ORGANISM: Pseudomonas jessenii 161 strain
US-10-133-404A-1
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Query Match

72.0%; Score 1098.6; DB 15; Length 1501;

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Best Local Similarity 85.9%; Pred. No. 1.2e-288;
Matches 1287; Conservative 0; Mismatches 202; Indels 9; Gaps 6;
Qy 30 GCGCGCAGGCTTAACACATGCAAGTCGAGCGGAACGATAGTAGCTTCTGATTAGCGTC 89
Db 9 GCGCGCAGGCTTAACACATGCAAGTCGAGCGG--ATGACGGGAGCTTCTCTCTGAATTCA 66
Qy 90 GAGCNGCGGACGGGTGAGTAAATCTTAGGAAATCTACCTAGTAGTGGGGGATAGTCGGG 149
Db 67 G---CGGCGGACGGGTGAGTAAATGCTTAGGAAATCTGCTTGTAGTGGGGGACAACTCTC 123
Qy 150 GAAACTCGAAATTAATACCGCATACGT-CTACGGGAGAAAGCAGGCGGNTCATTTAGACCTTG 208
Db 124 GAAAGGAGCGCTAATACCGCATACGTCTCTACGGGAGAAAGCAGGCGGACCTTCGGGCTTG 183
Qy 209 CGCTATTAGATGACCTTAAGTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTC 268
Db 184 CGCTATCAGATGACCTTAGGTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTC 243
Qy 269 ACATCTCTAGCTCTGAGAGGATGATCAGCCACACCGGACCTGAGACACGCGCCCGGA 328
Db 244 ACATCTCTAGCTCTGAGAGGATGATCAGCTCAGCTCAGCTCAGCTCAGCTCAGCTCAGCTC 303
Qy 329 CT-CTACGGGAGGACGATGCGGAAATATTGGAACAATGNGGGGAACCTCTGATCCAGCCAT 387
Db 304 CTCTACGGGAGGACGATGCGGAAATATTGGAACAATGNGGGGAACCTCTGATCCAGCCAT 363
Qy 388 GCGCGTGTGTGAAGAGGCTTTTGGTGTAAAGCACTTTAAGCAGTGAAGAGACTCT 447
Db 364 GCGCGTGTGTGAAGAGGCTTTTGGTGTAAAGCACTTTAAGTGTGGAGGAAGGGCAT 423
Qy 448 TCGGTTAATACCCGGGACGATGATCAGCTGAGAAATAGACACCGGCTTAACCTCTGTGC 507
Db 424 TAACTAATAGCTTAGTGTGTTGAGCTTACCGACAGATAGACCGGCTTAACCTCTGTGC 483
Qy 508 CAGCAGCGCGGTAAATACAGAGGTGCAAGCGTTAATCGGAATTAATCGGCGGTAAAGCGA 567
Db 484 CAGCAGCGCGGTAAATACAGAGGTGCAAGCGTTAATCGGAATTAATCGGCGGTAAAGCGC 543
Qy 568 GCGTAGTGGCTTCAATGATGAGTGAATCCCGGCTTAACCTGGGAACTGCACTCT 627
Db 544 GCGTAGTGGCTTCAATGATGAGTGAATCCCGGCTTAACCTGGGAACTGCACTCT 603
Qy 628 GAAACTGTTAGCTTAGTGTGAGGAAAGTAGAATTTTCAAGTGTAGCGGTGAAATG 687
Db 604 AAACTGCAAGCTTAGTGTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTT 663
Qy 688 CGTAGATCTGAAGGAATACCGATGCGGAAGGAGGCTTCTGGAATCATACTGACACTG 747
Db 664 CGTAGATCTGAAGGAATACCGATGCGGAAGGAGGCTTCTGGAATCATACTGACACTG 723
Qy 748 AGGCTCGAAAGCGTGGGTAGCAAAACAGGATTAGATACCTGGTAGTCCACCGCTAAACG 807
Db 724 AGGTCGCAAGCGTGGGTAGCAAAACAGGATTAGATACCTGGTAGTCCACCGCTAAACG 783
Qy 808 ATGTCTACTAGTCTGGGTCCCTTGGAGCTTAGTGAACGAGCTTAACCGCAATTAAGTGA 867
Db 784 ATGTCAACTAGCTTGGGACCTTGGCTCTTAGTGGCGAGCTTAACCGCAATTAAGTGA 843
Qy 868 CCGCTCTGGGAGTACCGCCGCAAGGTTAAAACTCAAAATGAATGACGGGGCCCGCACAA 927
Db 844 CCGCTCTGGGAGTACCGCCGCAAGGTTAAAACTCAAAATGAATGACGGGGCCCGCACAA 903
Qy 928 GCGGTGAGCATGTGTTTAAATTCGATGCAACCGCAAGAACCTTACCTGGTCTTGACATA 987
Db 904 GCGGTGAGCATGTGTTTAAATTCGATGCAACCGCAAGAACCTTACCTGGTCTTGACATC 963
Qy 988 CACAGAACTTTGTAGAGATACGAGGTGCTTCCGGGAATTTGTATACAGGTGCTCATGG 1047
Db 964 CAATGAACCTTTCCAGAGATGAGTGGTGGCTTCCGGGAACATTTGACAGAGGTGCTCATGG 1023
Qy 1048 CTGTGCTCAGCTCGTGTGAGATGTTGGTGTAAAGTCCCGCAACGAGCGCAACCTCTGT 1107
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Db 1384 AGTGGGTGCACAGAGTAGTCTAACCCTTCGGGAGGACGGTTACACGGGTGTGAT 1443  
Qy 1466 CGATGACTGGGGTGAAGTCGTAAACAGGTAGCCGTAGGGGAAACCTCGCGGTGGATCAC 1523  
Db 1444 TCATGACTGGGGTGAAGTCGTAAACAGGTAGCCGTAGGGGAAACCTCGCGGTGGATCAC 1501  
RESULT 15  
US-10-649-646-1  
; Sequence 1, Application US/10649646  
; Publication No. US20040067576A1  
; GENERAL INFORMATION:  
; APPLICANT: Canon Inc.  
; TITLE OF INVENTION: Polyhydroxynate, Method For Production Thereof And Microorganisms  
; TITLE OF INVENTION: In The Same  
; FILE REFERENCE: 03500.015001.2  
; CURRENT APPLICATION NUMBER: US/10/649,646  
; CURRENT FILING DATE: 2003-08-28  
; PRIOR FILING DATE: 1999-12-27 JP 11-371863  
; PRIOR APPLICATION NUMBER: JP 2000-023078  
; PRIOR FILING DATE: 2000-01-31  
; PRIOR APPLICATION NUMBER: JP 2000-023080  
; PRIOR FILING DATE: 2000-01-31  
; PRIOR APPLICATION NUMBER: JP 2000-023083  
; PRIOR FILING DATE: 2000-01-31  
; PRIOR APPLICATION NUMBER: JP 2000-095011  
; PRIOR FILING DATE: 2000-03-30  
; PRIOR APPLICATION NUMBER: JP 2000-095012  
; PRIOR FILING DATE: 2000-03-30  
; PRIOR APPLICATION NUMBER: JP 2000-095013  
; PRIOR FILING DATE: 2000-03-30  
; PRIOR APPLICATION NUMBER: JP 2000-207089  
; PRIOR FILING DATE: 2000-07-07  
; PRIOR APPLICATION NUMBER: JP 2000-207091  
; PRIOR FILING DATE: 2000-07-07  
; PRIOR APPLICATION NUMBER: JP 2000-359789  
; PRIOR FILING DATE: 2000-11-27  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 1  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 1501  
; TYPE: DNA  
; ORGANISM: Pseudomonas jessenii 161 strain  
US-10-649-646-1  
Query Match 72.0%; Score 1098.6; DB 17; Length 1501;  
Best Local Similarity 85.9%; Pred. No. 1.2e-288;  
Matches 1287; Conservative 0; Mismatches 202; Indels 9; Gaps 6;  
Qy 30 GCGGCGAGGCTTAACATGCAAGTCGAGCGGAAACGATGATGCTTGTATTAGGCGTC 89  
Db 9 GCGGCGAGGCTTAACATGCAAGTCGAGCGG--ATGACGGGAGCTTGTCTCTGAATTCA 66  
Qy 90 GAGCNGCGGCGGCTGAGTAATCTAGTAATCTAGTCTAGTGGGGATGCTCGGG 149  
Db 67 G---CGGCGGAGCGGTGAGTAATCTGCTAGGAATCTGCTGGTAGTGGGGACAACTGTC 123  
Qy 150 GAAACTCGAATTAATACCGCATAGCT-CTACGGGAGAAAGCAGGGGNTCAATTAGACCTTG 208  
Db 124 GAAAGGACGCTAATACCGCATAGCTCTACGGGAGAAAGCAGGGGACCTTCGGGCTTG 183  
Qy 209 CGCTATTAGATGACCTTAAGTCGAGTATGCTGGGTAAAGCCCTACCATGGCG 268  
Db 184 CGCTATCAGATGACCTTAGTTCGAGTATGCTGGGTAAAGCCCTACCAAGGCG 243  
Qy 269 ACNATCTGAGCTGCTGAGAGATGATCAGCCACACCGGACTGAGACACCGCCGGA 328  
Db 244 ACNATCTGAGCTGCTGAGAGATGATCAGTACACTGGAATGAGACACCGGTCAGA 303  
Qy 329 CT-CTACGGGAGGCGAGTCAGTGGGGAATATTGGACAATGCGGGAAACCTGATCCAGCCAT 387

Db 304 CTCTACGGGAGGACGAGTGGGGAATATTGGACAATGGCGAAAGCCTGATCCAGCCAT 363  
Qy 388 GCCGCGTGTGTGAAGAAGGCTTTTGGTTGTAAGCACATTTAAAGCAGTGAAGAAGACTCT 447  
Db 364 GCCGCGTGTGTGAAGAAGGCTTTCCGATTGTAAGCACATTTAAAGTTGGGAGGAAGGCGAT 423  
Qy 448 TCGTTTAATACCCGGGACGATGACATTAAGTTCAGAAATAGCACACCGGCTAACTCTGTGC 507  
Db 424 TAACTTAATACGTTAGTGTGTTTACGTTTACCGACAGAAATAGCACCGGCTAACTCTGTGC 483  
Qy 508 CAGCAGCCGCGTAAATACAGAGGGTGCAGAGCGTTAAATCGGAATTACTGGCGCTGAAGCGA 567  
Db 484 CAGCAGCCGCGTAAATACAGAGGGTGCAGAGCGTTAAATCGGAATTACTGGCGCTGAAGCGC 543  
Qy 568 GCCTAGGTGGCTTGTATAGTTCAGATGTGAATCCCGGGCTTAACTGGGAACTGATCT 627  
Db 544 GCCTAGGTGGTGTGTTTAAAGTTGATGTGAAGCCCGGGCTCAACTGGGAACTGCATTC 603  
Qy 628 GAACTGTTAGCTAGAGTAGGTGAGAGGAGTAGAATTTACAGGTGTAGCGTGAAATG 687  
Db 604 AAACTGACAAGCTAGAGTATGTAGAGGTGTGGAATTTCTGTGTAGCGTGAAATG 663  
Qy 688 CGTAGAGATCTGAAGGAATACCGATGGCGAAGGACGCTTCTTGGCATCATCTACTGACACTG 747  
Db 664 CGTAGATATAGGAAGGACACCACTGCGAAGGCGACCACTGGACTGATACTGACACTG 723  
Qy 748 AGCTCGAAGCGTGGGTAGCAACAGGATTAGATACCTTGGTAGTCCACCGCTGAACG 807  
Db 724 AGGTGCGAAGCGTGGGAGCAACAGGATTTAGATACCTTGGTAGTCCACCGCTGAACG 783  
Qy 808 ATGCTCTAGTGTGGTCCCTTCAGGACTTAGTGACGACGTAACGCAATTAAGTAGA 867  
Db 784 ATGCTCAACTAGCGTTGGGAGCCTTGAGCTCTTAGTGGCGACGTAACGATTAAGTTGA 843  
Qy 868 CCGCTCTGGGAGTACGCGCGCAAGGTTAAAACTCAATGAATTAAGCGGGGCGCCGACAA 927  
Db 844 CCGCTCTGGGAGTACGCGCGCAAGGTTAAAACTCAATGAATTAAGCGGGGCGCCGACAA 903  
Qy 928 GCGGTGGAGCATGTGTTTAAATTCGAAGCAACGCGAAGAACCTTACGAGCCTTGACATC 987  
Db 904 GCGGTGGAGCATGTGTTTAAATTCGAAGCAACGCGAAGAACCTTACGAGCCTTGACATC 963  
Qy 988 CACAGAACTTTGTAGAGATACGAGAGTGTCTTCGGGAATTTGTATACAGGTGTGATGG 1047  
Db 964 CAATGAACCTTTCCAGAGATGGATGGGTGCTTCGGGAACATTTGAGACAGGTGTGATGG 1023  
Qy 1048 CTGCTCAGCTCGTGTCTGTGAGATTTGGGTTAAGTCCCGCAACGAGCGCAACCTTGT 1107  
Db 1024 CTGCTCAGCTCGTGTCTGTGAGATTTGGGTTAAGTCCCGTAACGAGCGCAACCTTGT 1083  
Qy 1108 CTTAGTTACAGCAC- TTCCGGGTGGAACTCTAAGGATCTGCCAGTGAACAACTGGAG 1166  
Db 1084 CTTAGTTACAGCACGTAATGGTGGGCACTCTAAGGAGACTGCCGGTGAACAAACCGGAG 1143  
Qy 1167 GAAGCGGGGACGACGCTCAAGTCAATCGCCCTTACGACCGGGCTACACAGCTGCTAC 1226  
Db 1144 GAAGGTGGGATGACGTCAAGTCAATCGCCCTTACGGCTTGGGCTACACAGTGTCTAC 1203  
Qy 1227 AATGGTAGGTACAGAGGCGAGCTTACACAGCGATGTGATCGGAATCTCAAAAGCCATCG 1286  
Db 1204 AATGGTGGTACAGAGGGTTTCCAAAGCGCGAGGTGGAGCTAATCCACAAAACCGATCG 1263  
Qy 1287 TAGTCAGATTGGAGTCTGCAACTCCACTCCATGAAGTAGGATCGCTAGTAATCCGGA 1346  
Db 1264 TAGTCGCGATCGCAGTCTGCAACTCGGTAAGTGGGAATCGCTAGTAATCGGAA 1323  
Qy 1347 TCAGAAATCGCGGCTGAATACAGTTCCCGGCGCTTTGTACACACCGCCGCTCACACCTGGG 1406  
Db 1324 TCAGAAATCGCGGCTGAATACAGTTCCCGGCGCTTTGTACACACCGCCGCTCACACCTGGG 1383  
Qy 1407 AGTTGATTGCACAGAAAGTGGTTAGCCTAA-CTTAGTGGAGGCGATCAACACCGGTGTGT 1465

Db 1384 AGTGGTTGCACGAGTAGCTAGTCTAACCTTCGGGAGGACGGTTACCA CGGTGTGAT 1443  
Qy 1466 CGATGACTGGGTGAAGTCGTAAACAAGGTAGCCGTAGGGGAACCTGCGGCTGCATCAC 1523  
Db 1444 TCATGACTGGGTGAAGTCGTACCAAGGTAGCCGTAGGGGAACCTGCGGCTGCATCAC 1501

Search completed: April 12, 2005, 09:03:37  
Job time : 1140.89 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: April 12, 2005, 05:59:04 ; Search time 234 Seconds  
(without alignments)  
480.663 Million cell updates/sec

Title: US-09-979-558a-1\_COPY\_458\_476

Perfect score: 19

Sequence: 1 cccggggacgatgacatta 19

Scoring table: IDENTITY\_NUC

Gapop 10.0, Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N\_Geneseq\_16Dec04.\*

1: Geneseqn1980s.\*

2: Geneseqn1990s.\*

3: Geneseqn2000s.\*

4: Geneseqn2001as.\*

5: Geneseqn2001bs.\*

6: Geneseqn2002as.\*

7: Geneseqn2002bs.\*

8: Geneseqn2003as.\*

9: Geneseqn2003bs.\*

10: Geneseqn2003cs.\*

11: Geneseqn2003ds.\*

12: Geneseqn2004as.\*

13: Geneseqn2004bs.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
C 1	19	100.0	19	4 AAC87532	AAC87532 Psychroba
C 2	19	100.0	1526	4 AAC87531	AAC87531 Psychroba
C 3	16.4	86.3	86	11 ADM44619	Adm44619 Insect re
C 4	16.4	86.3	218	11 ADM44620	Adm44620 Insect re
C 5	16.4	86.3	584	3 AAC76269	AAC76269 Human ORF
C 6	16.4	86.3	1882	3 AAF21914	AAF21914 Human bre
C 7	16.4	86.3	1926	4 ABA06572	ABA06572 Human cDN
C 8	16.4	86.3	1926	6 ABV83909	ABV83909 Human pol
C 9	16.4	86.3	1987	3 AAZ52368	AAZ52368 NSEQ gene
C 10	16.4	86.3	1987	6 AAL42464	AAL42464 Human mat
C 11	16.4	86.3	1989	3 AAA37044	AAA37044 Human PRO
C 12	16.4	86.3	1989	4 AAF54255	AAF54255 DNA encod
C 13	16.4	86.3	1989	9 ACD68292	ACD68292 Novel hum
C 14	16.4	86.3	1989	9 ACH04394	ACH04394 Human cDN
C 15	16.4	86.3	1989	9 ACD67938	ACD67938 Novel hum
C 16	16.4	86.3	1989	10 ADC17945	ADC17945 Human PRO
C 17	16.4	86.3	1989	10 ADD70591	ADD70591 Human cDN
C 18	16.4	86.3	1989	10 ADD39668	ADD39668 Human cDN
C 19	16.4	86.3	1989	10 ADD70114	ADD70114 Human cDN
C 20	16.4	86.3	1989	10 ADD38235	ADD38235 Human cDN

C 21	16.4	86.3	1989	10 ADD39191	Add39191 Human cDN
C 22	16.4	86.3	1989	10 ADD38714	Add38714 Human cDN
C 23	16.4	86.3	1989	10 ADD40145	Add40145 Human cDN
C 24	16.4	86.3	1989	10 ADE50366	AdE50366 Human cDN
C 25	16.4	86.3	1989	10 ADE19978	AdE19978 Human cDN
C 26	16.4	86.3	1989	10 ADE49889	AdE49889 Human cDN
C 27	16.4	86.3	1989	10 ADE21447	AdE21447 Human cDN
C 28	16.4	86.3	1989	10 ADF29872	AdF29872 Human cDN
C 29	16.4	86.3	1989	10 ADF55765	AdF55765 Human cDN
C 30	16.4	86.3	1989	10 ADH99269	AdH99269 Human cDN
C 31	16.4	86.3	1989	12 ADE96449	AdE96449 Human cDN
C 32	16.4	86.3	1989	12 ADF25760	AdF25760 Human cDN
C 33	16.4	86.3	1989	12 ADF24659	AdF24659 Human cDN
C 34	16.4	86.3	1989	12 ADF29395	AdF29395 Human cDN
C 35	16.4	86.3	1989	12 ADE96926	AdE96926 Human cDN
C 36	16.4	86.3	1989	12 ADH02964	AdH02964 Human cDN
C 37	16.4	86.3	1989	12 ADH03918	AdH03918 Human cDN
C 38	16.4	86.3	1989	12 ADH03441	AdH03441 Human cDN
C 39	16.4	86.3	1989	12 ADH04395	AdH04395 Human cDN
C 40	16.4	86.3	1989	12 ADH61396	AdH61396 Human cDN
C 41	16.4	86.3	1989	12 ADL94595	AdL94595 Human cDN
C 42	16.4	86.3	1990	3 AAC58113	AAC58113 Human PRO
C 43	16.4	86.3	2005	4 AAH13666	AAH13666 Human cDN
C 44	16.4	86.3	2029	10 ADI21368	ADI21368 Novel hum
C 45	16.4	86.3	2040	11 ACN89680	ACN89680 Breast ca

ALIGNMENTS

RESULT 1

AAC87532/c

ID AAC87532 standard; DNA; 19 BP.

XX AAC87532;

XX 13-MAR-2001 (first entry)

XX Psychrobacter pacificensis 16S rDNA probe, SEQ ID NO:2.

DE 16S rDNA; species-specific detection; identification;

KW psychrophilic bacterium; oceanic circulation; Psychrobacter; probe; ss.

XX Psychrobacter pacificensis.

XX WO200071705-A1.

XX 30-NOV-2000.

XX 25-MAY-2000; 2000WO-JP003372.

XX 25-MAY-1999; 95JP-00145342.

PR 30-MAR-2000; 2000WO-JP002045.

XX (AGEN ) AGENCY OF IND SCI & TECHNOLOGY.

XX Maruyama A, Kitamura K, Kurane R;

XX WPI; 2001-025158/03.

DNA probe originating from psychrotrophic bacterium applicable in species-specific detection of the microorganism as indication in studying and monitoring its growth and circulation of deep-sea water with sensitivity.

Claim 3; Page 10; 37pp; Japanese.

The invention relates to a 1526 bp Psychrobacter pacificensis 16S rDNA sequence (AAC87531) and an oligonucleotide probe (AAC87532) comprising part of the Psychrobacter pacificensis 16S rDNA sequence which are used for monitoring the growth of psychrophilic bacteria and the circulation of deep-sea water. Psychrobacter pacificensis is an aerobic, Gram-negative, non-motile, non-spore-forming oxidase-positive bacterium originally isolated from the Japan Trench. The invention also relates to

CC a novel method for detecting or specifically identifying Psychrobacter  
 CC pacificensis, Psychrobacter glacincola, and related species, or  
 CC Psychrobacter pacificensis only via the use of the 16S rDNA sequence. The  
 CC 16S rDNA sequence and derived oligonucleotide probe are useful for the  
 CC species-specific detection of Psychrobacter pacificensis to study and  
 CC monitor its growth as an indicator of the circulation of deep-sea water.  
 CC The method of the invention is rapid, accurate and has high sensitivity,  
 CC and removes the need to separate and culture the biological materials.  
 CC The present sequence represents a specifically claimed Psychrobacter  
 CC pacificensis 16S rDNA oligonucleotide probe  
 XX  
 SQ Sequence 19 BP; 3 A; 6 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 4; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 8.3;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGGGGACGATGACATTA 19  
 |||||  
 Db 19 CCGGGGACGATGACATTA 1

## RESULT 2

AAC87531  
 ID AAC87531 standard; DNA; 1526 BP.

XX AC AAC87531;

XX DT 13-MAR-2001 (first entry)

XX DE Psychrobacter pacificensis NIBH P2K6 16S rDNA, SEQ ID NO:1.

XX KW 16S rDNA; species-specific detection; identification;  
 KW psychrophilic bacterium; oceanic circulation; Psychrobacter;  
 KW strain NIBH P2K6; ds.

XX OS Psychrobacter pacificensis.

XX PN W0200071705-A1.

XX PD 30-NOV-2000.

XX PF 25-MAY-2000; 2000WO-JP003372.

XX PR 25-MAY-1999; 99JP-00145342.

XX PR 30-MAR-2000; 2000WO-JP002045.

XX PA (AGEN ) AGENCY OF IND SCI & TECHNOLOGY.

XX PI Maruyama A, Kitamura K, Kurane R;

XX DR WPI; 2001-025158/03.

XX PT DNA probe originating from psychrotrophic bacterium applicable in species  
 PT -specific detection of the microorganism as indication in studying and  
 PT monitoring its growth and circulation of deep-sea water with sensitivity.

XX PS Claim 1; Page 30; 37pp; Japanese.

XX SQ The invention relates to a 1526 bp Psychrobacter pacificensis 16S rDNA  
 CC sequence (AAC87531) and an oligonucleotide probe (AAC87532) comprising  
 CC part of the Psychrobacter pacificensis 16S rDNA sequence which are used  
 CC for monitoring the growth of psychrophilic bacteria and the circulation  
 CC of deep-sea water. Psychrobacter pacificensis is an aerobic, Gram-  
 CC negative, non-motile, non-spore-forming oxidase-positive bacterium  
 CC originally isolated from the Japan Trench. The invention also relates to  
 CC a novel method for detecting or specifically identifying Psychrobacter  
 CC pacificensis, Psychrobacter glacincola, and related species, or  
 CC Psychrobacter pacificensis only via the use of the 16S rDNA sequence. The  
 CC 16S rDNA sequence and derived oligonucleotide probe are useful for the  
 CC species-specific detection of Psychrobacter pacificensis to study and  
 CC monitor its growth as an indicator of the circulation of deep-sea water.  
 CC The method of the invention is rapid, accurate and has high sensitivity,

CC and removes the need to separate and culture the biological materials.  
 CC The present sequence represents the Psychrobacter pacificensis 16S rDNA  
 XX  
 SQ Sequence 1526 BP; 401 A; 332 C; 467 G; 323 T; 0 U; 3 Other;

Query Match 100.0%; Score 19; DB 4; Length 1526;  
 Best Local Similarity 100.0%; Pred. No. 12;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGGGGACGATGACATTA 19  
 |||||  
 Db 458 CCGGGGACGATGACATTA 476

## RESULT 3

ADM44619

ID ADM44619 standard; DNA; 86 BP.

XX AC ADM44619;

XX DT 03-JUN-2004 (first entry)

XX DE Insect resistance associated N benthamiana DNA SeqID26.

XX KW insect resistant phenotype; plant protectant; gene therapy;  
 KW Arabidopsis thaliana; Nicotiana benthamiana; Oryza sativa;  
 KW Papaver rhoeas; rice; insect resistance; insect-resistant plant; ds.

XX OS Nicotiana benthamiana.

XX PN W02003020025-A2.

XX PD 13-MAR-2003.

XX PF 30-AUG-2002; 2002WO-US027882.

XX PR 31-AUG-2001; 2001US-0316319P.

XX PA (DOWC ) DOW CHEM CO.

XX PI Shukla V, Meade T, Larrinua I;

XX DR WPI; 2003-290133/28.

XX PT New isolated nucleic acid having expression that results in an insect  
 PT resistant phenotype, useful for conferring insect resistance and for  
 PT producing insect-resistant plants.

XX PS Claim 1; SEQ ID NO 26; 396pp; English.

XX SQ This invention relates to a novel isolated nucleic acid comprising, or  
 CC hybridising under low stringent conditions to, any of the 1214 nucleic  
 CC acid sequences given in the specification, where the expression of the  
 CC nucleic acid in a plant results in an insect resistant phenotype. The  
 CC invention may be useful as a plant protectant or for gene therapy. The  
 CC genes are derived from Arabidopsis thaliana, Nicotiana benthamiana, Oryza  
 CC sativa and Papaver rhoeas. The isolated nucleic acid and vector are  
 CC useful for conferring insect resistance and for producing insect-  
 CC resistant plants. The present sequence is that of a DNA sequence of the  
 CC invention which may confer insect resistance to plants.

XX SQ Sequence 86 BP; 24 A; 16 C; 26 G; 20 T; 0 U; 0 Other;

Query Match 86.3%; Score 16.4; DB 11; Length 86;  
 Best Local Similarity 94.4%; Pred. No. 1.9e+02;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CCGGGGACGATGACATTA 19  
 |||||  
 Db 11 CCGGGGACGATGACATTA 28

## RESULT 4

```

ADM44620
ID   ADM44620 standard; DNA; 218 BP.
XX
AC   ADM44620;
XX
DT   03-JUN-2004 (first entry)
XX
DE   Insect resistance associated N benthamiana DNA SeqID27.
XX
KW   insect resistant phenotype; plant protectant; gene therapy;
KW   Arabidopsis thaliana; Nicotiana benthamiana; Oryza sativa;
KW   Papaver rhoeas; rice; insect resistance; insect-resistant plant; ds.
XX
OS   Nicotiana benthamiana.
XX
PN   WO2003020025-A2.
XX
PD   13-MAR-2003.
XX
PF   30-AUG-2002; 2002WO-US027882.
XX
PR   31-AUG-2001; 2001US-0316319P.
XX
PA   (DOWC ) DOW CHEM CO.
XX
PI   Shukla V, Meade T, Larrinua I;
XX
WPI: 2003-290133/28.
XX
PT   New isolated nucleic acid having expression that results in an insect
PT   resistant phenotype, useful for conferring insect resistance and for
PT   producing insect-resistant plants.
XX
PS   Claim 1; SEQ ID NO 27; 396pp; English.
XX
CC   This invention relates to a novel isolated nucleic acid comprising, or
CC   hybridising under low stringent conditions to, any of the 1214 nucleic
CC   acid sequences given in the specification, where the expression of the
CC   nucleic acid in a plant results in an insect resistant phenotype. The
CC   invention may be useful as a plant protectant or for gene therapy. The
CC   genes are derived from Arabidopsis thaliana, Nicotiana benthamiana, Oryza
CC   sativa and Papaver rhoeas. The isolated nucleic acid and vector are
CC   useful for conferring insect resistance and for producing insect-
CC   resistant plants. The present sequence is that of a DNA sequence of the
CC   invention which may confer insect resistance to plants.
XX
SQ   Sequence 218 BP; 60 A; 28 C; 45 G; 85 T; 0 U; 0 Other;

Query Match      86.3%; Score 16.4; DB 11; Length 218;
Best Local Similarity 94.4%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy   2 CCGGGGACGATGACATTA 19
     |||||
Db   11 CCGGGGACGATGACATTA 28

RESULT 5
AAC76269/c
ID   AAC76269 standard; cDNA; 584 BP.
XX
AC   AAC76269;
XX
DT   08-FEB-2001 (first entry)
XX
DE   Human ORFX ORF1824 polynucleotide sequence SEQ ID NO:3647.
XX
KW   Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;
KW   vulnery; antiparasitic; antiparkinsonian; nootropic; neuroprotective;
KW   anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;
KW   immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
KW   hypotensive; dermatological; immunosuppressive; antiinflammatory;
KW   antiviral; antibacterial; antifungal; antirheumatic; antithyroid;

antianaemic; gene therapy; cancer; proliferative disorder; hypertension;
neurodegenerative disorder; osteoarthritis; graft vs host disease;
cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
cholesterol ester storage; systemic lupus erythematosus; infection;
severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
bone damage; cartilage damage; antiinflammatory disease; coagulation;
thrombosis; contraceptive; ss.

Homo sapiens.
WO200058473-A2.
05-OCT-2000.
31-MAR-2000; 2000WO-US008621.
31-MAR-1999; 99US-0127607P.
02-APR-1999; 99US-0127636P.
05-APR-1999; 99US-0127728P.
30-MAR-2000; 2000US-00540763.
(CURA-) CURAGEN CORP.
Shimkets RA, Leach M;
WPI: 2000-602362/57.
P-PSDB; AAB42060.

Novel nucleic acids and peptides derived from open reading frame X,
useful for treating e.g. cancers, proliferative disorders,
neurodegenerative disorders and cardiovascular disease.

Claim 5; Page 2803; 5507pp; English.

AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,
which represent the human ORFX open reading frames 1 to 3161. The ORFX
sequences have activities such as: cytostatic; hepatotropic; vulnery;
anticancer; antiparkinsonian; nootropic; neuroprotective; osteopathic;
anticonvulsant; antiarthritic; immunosuppressant; immunostimulant;
cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive;
dermatological; immunosuppressive; antiinflammatory; antibacterial;
antiviral; antifungal; antirheumatic; antithyroid; and antianaemic. The
sequences can be used for determining the presence of or predisposition
to, or preventing or treating pathological conditions associated with an
ORFX-associated disorder. The nucleic acids can be used to express ORFX
proteins in gene therapy vectors. The proteins can be used to express ORFX
used to treat cancers, proliferative disorders, neurodegenerative
disorders, osteoarthritis, graft vs host disease, cardiovascular disease,
diabetes mellitus, hypertension, hypothyroidism, cholesterol ester
storage, systemic lupus erythematosus, severe combined immunodeficiency
(SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune
disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and
cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to
enhance coagulation; to inhibit thrombosis; and as a contraceptive

Sequence 584 BP; 74 A; 232 C; 183 G; 93 T; 0 U; 2 Other;

Query Match      86.3%; Score 16.4; DB 3; Length 584;
Best Local Similarity 94.4%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy   1 CCGGGGACGATGACATT 18
     |||||
Db   497 CTCGGGACGATGACATT 480

RESULT 6
AAF21914/c
ID   AAF21914 standard; DNA; 1882 BP.
XX
AC   AAF21914;
XX

```

DT 27-MAR-2001 (first entry)  
 XX Human breast and ovarian cancer associated antigen gene SEQ ID 301.  
 DE  
 XX Human; breast cancer; ovarian cancer; cytostatic; immunosuppressive;  
 KW neotropic; neuroprotective; antiviral; antiallergic; hepatotropic;  
 KW antidiabetic; antiinflammatory; antitumor; vulnerary; anticonvulsant;  
 KW antibacterial; antifungal; antiparasitic; cardiant; immune disorder;  
 KW Addison's disease; allergy; autoimmune haemolytic anaemia;  
 KW autoimmune thyroiditis; diabetes mellitus; Crohn's disease;  
 KW multiple sclerosis; rheumatoid arthritis; ulcerative colitis;  
 KW cardiovascular disorder; wound healing; neurological disease; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200055173-A1.  
 XX  
 PD 21-SEP-2000.  
 XX  
 PF 08-MAR-2000; 2000WO-US005881.  
 XX  
 PP 12-MAR-1999; 99US-0124270P.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 XX Rosen CA, Ruben SM;  
 PI  
 XX WPI; 2000-611515/58.  
 DR  
 DR P-PSDB; AAB59011.  
 XX  
 XX New human breast and ovarian cancer associated gene sequences and the  
 PT polypeptides encoded by these genes, useful in the prevention, treatment  
 PT and diagnosis of cancer, immune disorders, cardiovascular disorders and  
 PT neurological diseases.  
 XX  
 PS Claim 1; Page 712-713; 1299pp; English.  
 XX  
 XX Sequences AAF22614 - AAF22031 represent DNA sequences encoding human  
 CC proteins AAB58711 - AAB59128. The DNA and protein sequences are  
 CC associated with breast and ovarian cancer. Included in the invention are  
 CC sequences AAF22032 - AAF22040 and AAB59129 which are used in the  
 CC isolation and characterisation of the DNA and protein sequences of the  
 CC invention. The breast and ovarian cancer associated DNA, protein, agonist  
 CC or antagonist sequences exhibit cytostatic; immunosuppressive; neotropic;  
 CC neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic;  
 CC antiinflammatory; antitumor; vulnerary; anticonvulsant; antibacterial;  
 CC antifungal; antiparasitic and cardiant activity. The polynucleotide and  
 CC protein sequences are used in the diagnosis of cancer, particularly  
 CC breast and ovarian cancer. The nucleic acid sequences, proteins, agonists  
 CC and agonists may also be used in the diagnosis, prevention and treatment  
 CC of immune disorders e.g. Addison's disease, allergies, autoimmune  
 CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's  
 CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis;  
 CC cardiovascular disorders such as myocardial ischaemias; wound healing;  
 CC neurological diseases such as cerebral anoxia and epilepsy; and  
 CC infectious diseases  
 XX  
 SQ Sequence 1882 BP; 383 A; 616 C; 527 G; 350 T; 0 U; 6 Other;  
 Query Match 86.3%; Score 16.4; DB 3; Length 1882;  
 Best Local Similarity 94.4%; Pred. No. 2.5e+07;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 CCCGGGGACGATGACATT 18  
 Db 546 CTCGGGGACGATGACATT 529  
 RESULT 7  
 ABA06572/c  
 ID ABA06572 standard; cDNA; 1926 BP.  
 XX  
 AC ABA06572;

XX 10-JAN-2002 (first entry)  
 DT  
 XX Human cDNA SEQ ID NO: 238.  
 DE  
 XX Human; gene therapy; neural disorder; immune system disorder;  
 KW muscular disorder; reproductive disorder; gastrointestinal disorder;  
 KW pulmonary disorder; cardiovascular disorder; renal disorder;  
 KW proliferative disorder; inflammation; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200154474-A2.  
 XX  
 PD 02-AUG-2001.  
 XX  
 PF 17-JAN-2001; 2001WO-US001349.  
 XX  
 PP 31-JAN-2000; 2000US-0179065P.  
 PR 04-FEB-2000; 2000US-0180628P.  
 PR 24-FEB-2000; 2000US-0184664P.  
 PR 02-MAR-2000; 2000US-0186350P.  
 PR 16-MAR-2000; 2000US-0189874P.  
 PR 17-MAR-2000; 2000US-0190076P.  
 PR 18-APR-2000; 2000US-0198123P.  
 PR 19-MAY-2000; 2000US-0205515P.  
 PR 07-JUN-2000; 2000US-0209467P.  
 PR 28-JUN-2000; 2000US-0214886P.  
 PR 30-JUN-2000; 2000US-0215135P.  
 PR 07-JUL-2000; 2000US-0216647P.  
 PR 07-JUL-2000; 2000US-0216880P.  
 PR 11-JUL-2000; 2000US-0217487P.  
 PR 11-JUL-2000; 2000US-0217496P.  
 PR 14-JUL-2000; 2000US-0218290P.  
 PR 26-JUL-2000; 2000US-0220963P.  
 PR 26-JUL-2000; 2000US-0220964P.  
 PR 14-AUG-2000; 2000US-0224518P.  
 PR 14-AUG-2000; 2000US-0224519P.  
 PR 14-AUG-2000; 2000US-0225113P.  
 PR 14-AUG-2000; 2000US-0225214P.  
 PR 14-AUG-2000; 2000US-0225266P.  
 PR 14-AUG-2000; 2000US-0225267P.  
 PR 14-AUG-2000; 2000US-0225268P.  
 PR 14-AUG-2000; 2000US-0225270P.  
 PR 14-AUG-2000; 2000US-0225447P.  
 PR 14-AUG-2000; 2000US-0225757P.  
 PR 14-AUG-2000; 2000US-0225758P.  
 PR 14-AUG-2000; 2000US-0225759P.  
 PR 18-AUG-2000; 2000US-0226279P.  
 PR 22-AUG-2000; 2000US-0226681P.  
 PR 22-AUG-2000; 2000US-0226686P.  
 PR 22-AUG-2000; 2000US-0227182P.  
 PR 23-AUG-2000; 2000US-0227009P.  
 PR 30-AUG-2000; 2000US-0228924P.  
 PR 01-SEP-2000; 2000US-0229287P.  
 PR 01-SEP-2000; 2000US-0229343P.  
 PR 01-SEP-2000; 2000US-0229344P.  
 PR 01-SEP-2000; 2000US-0229345P.  
 PR 03-SEP-2000; 2000US-0229509P.  
 PR 05-SEP-2000; 2000US-0229513P.  
 PR 06-SEP-2000; 2000US-0230437P.  
 PR 06-SEP-2000; 2000US-0230438P.  
 PR 08-SEP-2000; 2000US-0231242P.  
 PR 08-SEP-2000; 2000US-0231243P.  
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 PR 08-SEP-2000; 2000US-0231414P.  
 PR 08-SEP-2000; 2000US-0232080P.  
 PR 12-SEP-2000; 2000US-0232081P.  
 PR 14-SEP-2000; 2000US-0232397P.  
 PR 14-SEP-2000; 2000US-0232398P.  
 PR 14-SEP-2000; 2000US-0232399P.











CC The present invention relates to secreted and transmembrane proteins.  
CC These proteins and the DNA encoding them may be used as hybridization  
CC probes, in chromosome and gene mapping and in the generation of anti-  
CC sense RNA and DNA. They may also be used to generate either  
CC transgenic animals or knockout animals which are in turn useful for  
CC development and screening of therapeutically useful reagents. The nucleic  
CC acids may also be used in gene therapy

SQ Sequence 1989 BP; 340 A; 693 C; 586 G; 370 T; 0 U; 0 Other;

Query Match 86.3%; Score 16.4; DB 4; Length 1989;  
Best Local Similarity 94.4%; Pred. No. 2.5e-02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 CCCGGGACGATGACATT 18  
Db 732 CTCGGGACGATGACATT 715

RESULT 13  
ACD68292/c  
ID ACD68292 standard; cDNA; 1989 BP.

XX ACD68292;

XX 17-SEP-2003 (first entry)

DE Novel human secreted and transmembrane protein PRO1293 cDNA.

XX Human; secreted and transmembrane protein; PRO; angiogenesis;  
KW endothelial cell proliferation; wound healing; immune response;  
KW T-lymphocytes proliferation; neonatal heart hypertrophy; tumour;  
KW cardiac insufficiency disorder; calcium flux; inflammation;  
KW vascular endothelial growth factor-stimulated proliferation;  
KW mammalian kidney mesangial cell proliferation; Berger disease;  
KW nephropathy; Schlemmer-Henoch purpura; celiac disease; Crohn's disease;  
KW dermatitis herpetiformis; diabetes; haemoglobin switch; insulinaemia;  
KW pancreatic beta-cell precursor cell differentiation; thalassemias;  
KW obesity; auditory hair cell regeneration; hearing loss; bone disorder;  
KW cartilage disorder; sports injury; arthritis; gene; ss.

XX Homo sapiens.

XX US2003073130-A1.

XX 17-APR-2003.

XX 11-DEC-2001; 2001US-00015869.

XX 01-SEP-1998; 98US-0098716P.  
PR 01-SEP-1998; 98US-0098723P.  
PR 01-SEP-1998; 98US-0098749P.  
PR 01-SEP-1998; 98US-0098750P.  
PR 02-SEP-1998; 98US-0098803P.  
PR 02-SEP-1998; 98US-0098821P.  
PR 02-SEP-1998; 98US-0098843P.  
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PR 17-SEP-1998; 98US-0100711P.  
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PR 22-OCT-1998; 98US-0105266P.  
PR 26-OCT-1998; 98US-0105693P.  
PR 26-OCT-1998; 98US-0105694P.  
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PR 28-OCT-1998; 98US-0106178P.  
PR 29-OCT-1998; 98US-0106248P.  
PR 29-OCT-1998; 98US-0106384P.  
PR 29-OCT-1998; 98US-0108500P.

PT PRO1787 that modulate glucose or free fatty acid uptake by skeletal  
PT muscle cells, and are useful for treating diabetes, hyper- or hypo-

Query Match 86.3%; Score 16.4; DB 9; Length 1989;  
Best Local Similarity 94.4%; Pred. NO. 2.5e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCGGGGACGATGACATT 18  
Db 732 CTCGGGACGATGACATT 715

RESULT 14  
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ID ACH04394 standard; cDNA; 1989 BP.  
XX  
AC ACH04394;  
XX  
DT 01-OCT-2003 (first entry)  
XX  
DE Human cDNA encoding secreted/transmembrane protein PRO1293.  
XX  
KW Human; ss; gene; secreted protein; transmembrane protein; PRO; vulnary;  
KW cardiant; antidiabetic; anorectic; antiarthritic; angiogenesis; cancer;  
KW adrenal cortical capillary; endothelial cell growth; wound healing;  
KW stimulated T-lymphocyte proliferation; immune response suppression;  
KW neonatal heart hypertrophy; cardiac insufficiency disorder;  
KW vascular endothelial growth factor; inflammation; mononuclear cell;  
KW eosinophil; diabetes; obesity; or hyper-insulinaemia; hypo-insulinaemia;  
KW chondrocyte redifferentiation; bone disorder; cartilage disorder;  
KW sports injury; arthritis.  
XX  
OS Homo sapiens.  
XX  
PN US2003044841-A1.  
XX  
PD 06-MAR-2003.  
XX  
PF 06-DEC-2001; 2001US-00006856.  
XX  
PR 01-SEP-1998; 98US-0098716P.  
PR 01-SEP-1998; 98US-0098723P.  
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PR 01-SEP-1998; 98US-0098750P.  
PR 02-SEP-1998; 98US-0098803P.  
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PR 10-SEP-1998; 98US-0099816P.  
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PR 15-SEP-1998; 98US-0100390P.  
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PR 17-NOV-1998; 98US-0108779P.  
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PR 18-NOV-1998; 98US-0108848P.  
PR 18-NOV-1998; 98US-0108849P.  
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PR 18-NOV-1998; 98US-0108851P.  
PR 18-NOV-1998; 98US-0108852P.  
PR 18-NOV-1998; 98US-0108858P.  
PR 18-NOV-1998; 98US-0108904P.  
PR 20-DEC-1998; 98US-0113286P.  
PR 22-DEC-1998; 98US-0114223P.  
PR 05-JAN-1999; 99WO-US000106.  
PR 16-APR-1999; 99US-0129674P.  
PR 23-JUN-1999; 99US-0141037P.  
PR 20-JUL-1999; 99US-0144758P.  
PR 26-JUL-1999; 99US-0145698P.  
PR 01-SEP-1999; 99WO-US020111.  
PR 15-SEP-1999; 99WO-US021194.  
PR 29-OCT-1999; 99US-0162506P.  
PR 30-NOV-1999; 99WO-US028313.  
PR 02-DEC-1999; 99WO-US028551.  
PR 16-DEC-1999; 99WO-US030095.  
PR 05-JAN-2000; 2000WO-US000219.  
PR 06-JAN-2000; 2000WO-US000376.  
PR 11-FEB-2000; 2000WO-US003565.  
PR 18-FEB-2000; 2000WO-US004342.  
PR 24-FEB-2000; 2000WO-US005004.  
PR 02-MAR-2000; 2000WO-US005841.  
PR 15-MAR-2000; 2000WO-US006884.  
PR 17-MAY-2000; 2000WO-US013705.  
PR 22-MAY-2000; 2000WO-US014042.  
PR 30-MAY-2000; 2000WO-US014941.  
PR 02-JUN-2000; 2000WO-US015264.  
PR 23-AUG-2000; 2000WO-US023522.  
PR 08-NOV-2000; 2000WO-US030952.  
PR 10-NOV-2000; 2000WO-US030873.  
PR 01-DEC-2000; 2000WO-US032678.  
PR 28-FEB-2001; 2001WO-US006520.  
PR 01-MAR-2001; 2001WO-US006656.  
PR 01-JUN-2001; 2001WO-US017800.  
PR 20-JUN-2001; 2001WO-US019692.  
PR 29-JUN-2001; 2001WO-US021956.  
PR 09-JUL-2001; 2001WO-US021735.  
PR 04-SEP-2001; 2001US-00946374.

(GETH ) GENENTECH INC.  
PA  
XX  
XX Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;  
PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;  
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;  
PI Williams PM, Wood WI;  
XX  
XX WPI; 2003-585293/55.  
DR P-PSDB; ABO33604.  
XX  
XX Novel isolated PRO polypeptides e.g. PRO1130, PRO1275, PRO1418, PRO1555,  
PT

PR 17-SEP-1998; 98US-0100930P.  
PR 18-SEP-1998; 98US-0100848P.  
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PR 23-SEP-1998; 98US-0101471P.  
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PR 24-SEP-1998; 98US-0101913P.  
PR 24-SEP-1998; 98US-0101916P.  
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PR 30-SEP-1998; 98US-0102571P.  
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PR 01-OCT-1998; 98US-0102687P.  
PR 02-OCT-1998; 98US-0102965P.  
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PR 09-JUL-2001; 2001WO-US021735.  
PR 04-SEP-2001; 2001US-00946374.  
XX (GETH ) GENENTECH INC.  
XX Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;  
PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;  
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;  
PI Williams PM, Wood WI;  
XX WPI; 2003-492259/46.  
DR P-PSDB; ABO44457.  
XX  
PT Novel secreted and transmembrane polypeptides and polynucleotides  
PT encoding them useful for treating various cardiac insufficiency  
PT disorders, bone and/or cartilage disorders such as sports injuries and  
PT arthritis.  
Query Match 86.3%; Score 16.4; DB 9; Length 1989;  
Best Local Similarity 94.4%; Pred. No. 2.5e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCGGGGACGATGACATT 18  
Db 732 CTCGGGGACGATGACATT 715

RESULT 15  
ID ACD67938/c  
XX ACD67938 standard; cDNA; 1989 BP.  
XX AC ACD67938;  
XX DT 17-SEP-2003 (first entry)  
XX DE Novel human secreted and transmembrane protein PRO1293 cDNA.  
XX KW Human; secreted and transmembrane protein; PRO; gene therapy; vaccine;  
XX KW tissue typing; chromosome identification; vaccine; gene; ss.  
XX OS Homo sapiens.  
XX PN US2003073129-A1.  
XX PD 17-APR-2003.  
XX PF 04-SEP-2001; 2001US-00946374.  
XX PR 01-SEP-1998; 98US-0098716P.  
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PR 01-SEP-1998; 98US-0098749P.  
PR 01-SEP-1998; 98US-0098750P.  
PR 02-SEP-1998; 98US-0098803P.  
PR 02-SEP-1998; 98US-0098821P.  
PR 02-SEP-1998; 98US-0098843P.  
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PR 09-SEP-1998; 98US-0099596P.  
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PR 10-SEP-1998; 98US-0099763P.  
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PR 10-NOV-1998; 98US-0107783P.  
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

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Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

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Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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C 3	15.4	81.1	2338	4	US-09-582-337-1
C 4	15.4	81.1	2350	3	US-09-187-478-1
C 5	15.4	81.1	2350	3	US-09-292-036-1
C 6	15.4	81.1	51049	4	US-09-949-016-15571
C 7	15	78.9	636	4	US-09-902-540-8517
C 8	15	78.9	6855	4	US-09-902-540-897
C 9	14.8	77.9	99	1	US-08-427-097-12
C 10	14.8	77.9	99	2	US-08-878-957-12
C 11	14.8	77.9	170	1	US-08-419-078-5
C 12	14.8	77.9	170	1	US-08-419-078-6
C 13	14.8	77.9	170	1	US-08-726-883-5
C 14	14.8	77.9	170	1	US-08-726-883-6
C 15	14.8	77.9	300	1	US-08-419-078-4
C 16	14.8	77.9	300	1	US-08-726-883-4
C 17	14.8	77.9	384	4	US-09-389-681-451
C 18	14.8	77.9	384	4	US-09-620-405B-451
C 19	14.8	77.9	384	4	US-09-433-826B-451
C 20	14.8	77.9	384	4	US-09-604-287A-451
C 21	14.8	77.9	384	4	US-09-834-759-451
C 22	14.8	77.9	384	4	US-09-590-751A-451
C 23	14.8	77.9	384	4	US-09-551-621-451
C 24	14.8	77.9	879	4	US-09-248-796A-7856
C 25	14.8	77.9	1322	1	US-08-419-078-1
C 26	14.8	77.9	1322	1	US-08-726-883-1
C 27	14.8	77.9	1323	4	US-09-023-655-55

28	14.8	77.9	1594	4	US-09-270-767-14907	Sequence 14907, A
C 29	14.8	77.9	1752	1	US-08-427-097-13	Sequence 13, Appl
C 30	14.8	77.9	1752	1	US-08-427-097-19	Sequence 19, Appl
C 31	14.8	77.9	1752	2	US-08-878-957-13	Sequence 13, Appl
C 32	14.8	77.9	1752	2	US-08-878-957-19	Sequence 19, Appl
C 33	14.8	77.9	2936	4	US-09-976-594-1044	Sequence 1044, Ap
C 34	14.8	77.9	28843	4	US-09-949-016-17325	Sequence 17325, A
C 35	14.8	77.9	134987	4	US-09-949-016-15348	Sequence 15348, A
C 36	14.8	77.9	134987	4	US-09-949-016-15349	Sequence 15349, A
C 37	14.8	77.9	134987	4	US-09-949-016-15350	Sequence 15350, A
C 38	14.8	77.9	134987	4	US-09-949-016-15507	Sequence 15507, A
C 39	14.8	77.9	134987	4	US-09-949-016-15508	Sequence 15508, A
C 40	14.8	77.9	134987	4	US-09-949-016-15509	Sequence 15509, A
C 41	14.8	77.9	203475	4	US-09-949-016-14516	Sequence 14516, A
C 42	14.8	77.9	203475	4	US-09-949-016-14517	Sequence 14517, A
C 43	14.8	77.9	203475	4	US-09-949-016-14518	Sequence 14518, A
C 44	14.8	77.9	203475	4	US-09-949-016-14519	Sequence 14519, A
C 45	14.8	77.9	203475	4	US-09-949-016-17226	Sequence 17226, A

## ALIGNMENTS

### RESULT 1

US-09-552-322-1/c  
; Sequence 1, Application US/09552322  
; Patent No. 6436642  
; GENERAL INFORMATION:  
; APPLICANT: Gould-Rothberg  
; APPLICANT: Rastelli  
; TITLE OF INVENTION: METHOD OF CLASSIFYING A THYROID CARCINOMA USING  
; FILE REFERENCE: 15966-548  
; CURRENT APPLICATION NUMBER: US/09/552,322  
; CURRENT FILING DATE: 2000-04-19  
; PRIOR FILING DATE: 1999-04-20  
; PRIOR APPLICATION NUMBER: 60/193,203  
; PRIOR FILING DATE: 2000-03-30  
; NUMBER OF SEQ ID NOS: 63  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 2132  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-552-322-1

Query Match 86.3%; Score 16.4; DB 3; Length 2132;  
Best Local Similarity 94.4%; Pred. No. 78;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 CCCGGGGACGATGACATT 18  
Db 861 CTCGGGGACGATGACATT 844

### RESULT 2

US-09-949-016-136302/c  
; Sequence 136302, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08

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; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 136302
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-136302

Query Match      81.1%; Score 15.4; DB 4; Length 601;
Best Local Similarity 94.1%; Pred. No. 2.2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCGGGGACGATGACAT 17
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Db 77 CCCGGGGACATGACAT 61

RESULT 3
US-09-582-337-1
; Sequence 1, Application US/09582337
; Patent No. 6562618
; GENERAL INFORMATION:
; APPLICANT: Japan Tobacco, Inc.
; TITLE OF INVENTION: Monoclonal Antibody Against Connective Tissue Growth Factor
; FILE REFERENCE: J1-009PCT
; CURRENT APPLICATION NUMBER: US/09/582.337
; CURRENT FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: JP P1997-367699
; PRIOR FILING DATE: 1997-12-25
; PRIOR APPLICATION NUMBER: JP P1998-356183
; PRIOR FILING DATE: 1998-12-15
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2338
; TYPE: DNA
; ORGANISM: Rat
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: (1)..(212)
; NAME/KEY: CDS
; LOCATION: (213)..(1256)
; NAME/KEY: 3'UTR
; LOCATION: (1257)..(2338)
; NAME/KEY: polyA_signal
; LOCATION: (2297)..(2302)
US-09-582-337-1

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Db 1194 CCCGGGGACATGACAT 1210

RESULT 4
US-09-187-478-1
; Sequence 1, Application US/09187478
; Patent No. 6348329
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Brian F.
; APPLICANT: Allen, Margaret L.
; TITLE OF INVENTION: Connective Tissue Growth (CTGF) And Methods Of Use
; FILE REFERENCE: 08766/004001
; CURRENT APPLICATION NUMBER: US/09/187.478
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2350
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; TYPE: DNA
; ORGANISM: No. 6348329mal Rate Kidney Fibroblast
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (212)..(1252)
US-09-187-478-1

Query Match      81.1%; Score 15.4; DB 3; Length 2350;
Best Local Similarity 94.1%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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RESULT 5
US-09-292-036-1
; Sequence 1, Application US/09292036
; Patent No. 6358741
; GENERAL INFORMATION:
; APPLICANT: FIBROGEN, INC
; APPLICANT: SCHMIDT, Brian
; APPLICANT: ALLEN, Margaret
; APPLICANT: SVERDRUP, Fran
; APPLICANT: CARMICHAEL, David
; TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR (CTGF) AND METHODS OF USE
; FILE REFERENCE: FIBRO1100-1
; CURRENT APPLICATION NUMBER: US/09/292.036
; CURRENT FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: US 09/292,036
; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: US 09/187,478
; PRIOR FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 2350
; TYPE: DNA
; ORGANISM: Rat
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; NAME/KEY: CDS
; LOCATION: (212)..(1252)
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Query Match      81.1%; Score 15.4; DB 3; Length 2350;
Best Local Similarity 94.1%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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RESULT 6
US-09-949-016-15571
; Sequence 15571, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949.016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
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; SOFTWARE: FastSeq for Windows Version 4.0
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US-09-949-016-15571

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Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 13209 CCCGGGACGATGACAT 13225

## RESULT 7

US-09-902-540-8517  
; Sequence 8517, Application US/09902540  
; Patent No. 6833447  
; GENERAL INFORMATION:  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Wiegand, Roger C.  
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof  
; FILE REFERENCE: 38-10(15849)B  
; CURRENT APPLICATION NUMBER: US/09/902,540  
; CURRENT FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: 60/217,883  
; PRIOR FILING DATE: 2000-07-10  
; NUMBER OF SEQ ID NOS: 16825  
; SEQ ID NO 8517  
; LENGTH: 636  
; TYPE: DNA  
; ORGANISM: Myxococcus xanthus  
US-09-902-540-8517

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Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCGGGACGATGAC 15  
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Db 265 CCCGGGACGATGAC 279

## RESULT 8

US-09-902-540-897  
; Sequence 897, Application US/09902540  
; Patent No. 6833447  
; GENERAL INFORMATION:  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Wiegand, Roger C.  
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof  
; FILE REFERENCE: 38-10(15849)B  
; CURRENT APPLICATION NUMBER: US/09/902,540  
; CURRENT FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: 60/217,883  
; PRIOR FILING DATE: 2000-07-10  
; NUMBER OF SEQ ID NOS: 16825  
; SEQ ID NO 897  
; LENGTH: 6855  
; TYPE: DNA  
; ORGANISM: Myxococcus xanthus  
US-09-902-540-897

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Best Local Similarity 100.0%; Pred. No. 4.4e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 4043 CCCGGGACGATGAC 4057  
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## RESULT 9

US-08-427-097-12/c  
; Sequence 12, Application US/08427097  
; Patent No. 5668294  
; GENERAL INFORMATION:  
; APPLICANT: Meagher, Richard B.  
; APPLICANT: Sommers, Anne O.  
; TITLE OF INVENTION: Metal Resistance Sequences and  
; TITLE OF INVENTION: Transgenic Plants  
; NUMBER OF SEQUENCES: 30  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.  
; STREET: 5370 Manhattan Circle, Suite 201  
; CITY: Boulder  
; STATE: CO  
; COUNTRY: US  
; ZIP: 80303  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/427,097  
; FILING DATE: 21-APR-1995  
; CLASSIFICATION: 800  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ferber, Donna M.  
; REGISTRATION NUMBER: 33,878  
; REFERENCE/DOCKET NUMBER: 40-94  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (303) 499-8080  
; TELEFAX: (303) 499-8089  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 99 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
; DESCRIPTION: /desc = "Oligonucleotide"  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
US-08-427-097-12

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Best Local Similarity 88.9%; Pred. No. 3.8e+02;  
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Db 96 CCCGGGTCGATGACAATA 79

## RESULT 10

US-08-878-957-12/c  
; Sequence 12, Application US/08878957  
; Patent No. 5965796  
; GENERAL INFORMATION:  
; APPLICANT: Meagher, Richard B.  
; APPLICANT: Sommers, Anne O.  
; APPLICANT: Rugh, Clayton L.  
; TITLE OF INVENTION: Metal Resistance Sequences and  
; TITLE OF INVENTION: Transgenic Plants  
; NUMBER OF SEQUENCES: 34  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.  
; STREET: 5370 Manhattan Circle, Suite 201  
; CITY: Boulder

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COUNTRY: US
ZIP: 80303
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
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  FILING DATE: 19-JUN-1997
  CLASSIFICATION: 800
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US 08/427,097
    FILING DATE: 21-APR-1995
  ATTORNEY/AGENT INFORMATION:
    NAME: Ferber, Donna M.
    REGISTRATION NUMBER: 33,878
    REFERENCE/DOCKET NUMBER: 40-94A
  TELECOMMUNICATION INFORMATION:
    TELEPHONE: (303) 499-8080
    TELEFAX: (303) 499-8089
    TELEX:
  INFORMATION FOR SEQ ID NO: 12:
    SEQUENCE CHARACTERISTICS:
      LENGTH: 99 base pairs
      TYPE: nucleic acid
      STRANDEDNESS: single
      TOPOLOGY: linear
    MOLECULE TYPE: other nucleic acid
    DESCRIPTION: /desc = "Oligonucleotide"
    HYPOTHETICAL: NO
    ANTI-SENSE: NO
    US-08-878-957-12

Query Match          77.9%; Score 14.8; DB 2; Length 99;
Best Local Similarity 88.9%; Pred. No. 3.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCGGGGACGATGACATTA 19
Db 96 CCGGGGTCGATGACAA 79

RESULT 11
US-08-419-078-5
; Sequence 5, Application US/08419078
; Patent No. 5587306
; GENERAL INFORMATION:
; APPLICANT: HAWKINS, PHILLIP R.
; APPLICANT: SEILHAMER, JEFFREY J.
; TITLE OF INVENTION: PHOSPHOLIPASE C HOMOLOG
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3330 HILLVIEW AVENUE
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/419,078
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: LUTHER, BARBARA J.
; REGISTRATION NUMBER: 33954
; REFERENCE/DOCKET NUMBER: PF0030 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-855-0572
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 170 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; IMMEDIATE SOURCE:
; LIBRARY: Fibroblast
; CLONE: 054216
; US-08-419-078-6

Query Match          77.9%; Score 14.8; DB 1; Length 170;
Best Local Similarity 88.9%; Pred. No. 4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCGGGGACGATGACATT 18
Db 117 CCGGTGAGGATGACATT 134
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TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-855-0572
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 170 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; IMMEDIATE SOURCE:
; LIBRARY: Corneal Stroma
; CLONE: 046611
; US-08-419-078-5

Query Match          77.9%; Score 14.8; DB 1; Length 170;
Best Local Similarity 88.9%; Pred. No. 4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCGGGGACGATGACATT 18
Db 117 CCGGTGAGGATGACATT 134

RESULT 12
US-08-419-078-6
; Sequence 6, Application US/08419078
; Patent No. 5587306
; GENERAL INFORMATION:
; APPLICANT: HAWKINS, PHILLIP R.
; APPLICANT: SEILHAMER, JEFFREY J.
; TITLE OF INVENTION: PHOSPHOLIPASE C HOMOLOG
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3330 HILLVIEW AVENUE
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/419,078
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: LUTHER, BARBARA J.
; REGISTRATION NUMBER: 33954
; REFERENCE/DOCKET NUMBER: PF0030 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-855-0572
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 170 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; IMMEDIATE SOURCE:
; LIBRARY: Fibroblast
; CLONE: 054216
; US-08-419-078-6

Query Match          77.9%; Score 14.8; DB 1; Length 170;
Best Local Similarity 88.9%; Pred. No. 4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCGGGGACGATGACATT 18
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Db      117 CCCGTGGAGGATGACATT 134
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RESULT 13
US-08-726-883-5
; Sequence 5, Application US/08726883
; Patent No. 5676946
; GENERAL INFORMATION:
; APPLICANT: HAWKINS, PHILLIP R.
; APPLICANT: SEILHAMER, JEFFREY J.
; TITLE OF INVENTION: PHOSPHOLIPASE C HOMOLOG
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3330 HILLVIEW AVENUE
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/726,883
; FILING DATE: 04-OCT-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/419,078
; FILING DATE: 10-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: LUTHER, BARBARA J.
; REGISTRATION NUMBER: 33954
; REFERENCE/DOCKET NUMBER: PF0030 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-855-0572
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 170 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; IMMEDIATE SOURCE:
; LIBRARY: Fibroblast
; CLONE: 054216
; US-08-726-883-6

Query Match      77.9%; Score 14.8; DB 1; Length 170;
Best Local Similarity 88.9%; Pred. No. 4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 CCCGGGGACGATGACATT 18
|||||
Db      117 CCCGTGGAGGATGACATT 134
|||||

RESULT 15
US-08-419-078-4
; Sequence 4, Application US/08419078
; Patent No. 5587306
; GENERAL INFORMATION:
; APPLICANT: HAWKINS, PHILLIP R.
; APPLICANT: SEILHAMER, JEFFREY J.
; TITLE OF INVENTION: PHOSPHOLIPASE C HOMOLOG
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3330 HILLVIEW AVENUE
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/419,078
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: LUTHER, BARBARA J.
; REGISTRATION NUMBER: 33954
; REFERENCE/DOCKET NUMBER: PF0030 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-855-0572
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 170 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; IMMEDIATE SOURCE:
; LIBRARY: Corneal Stroma
; CLONE: 046611
; US-08-726-883-5

Query Match      77.9%; Score 14.8; DB 1; Length 170;
Best Local Similarity 88.9%; Pred. No. 4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 CCCGGGGACGATGACATT 18
|||||
Db      117 CCCGTGGAGGATGACATT 134
|||||

RESULT 14
US-08-726-883-6
; Sequence 6, Application US/08726883
; Patent No. 5676946
; GENERAL INFORMATION:
; APPLICANT: HAWKINS, PHILLIP R.
; APPLICANT: SEILHAMER, JEFFREY J.
; TITLE OF INVENTION: PHOSPHOLIPASE C HOMOLOG
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3330 HILLVIEW AVENUE
; CITY: PALO ALTO
```

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;
; TELEPHONE: 415-855-0555
; TELEFAX: 415-855-0572
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 300 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; LIBRARY: Hybrid T/B Lymphoblast
; CLONE: 043866
;
US-08-419-078-4

Query Match      77.9%; Score 14.8; DB 1; Length 300;
Best Local Similarity 88.9%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 CCGGGGACGATGACATT 18
        |||||
Db       239 CCGGTGGAGGATGACATT 256
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Search completed: April 12, 2005, 10:01:56  
Job time : 90 secs



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: April 12, 2005, 09:31:24 ; Search time 289 Seconds  
(without alignments)  
398.409 Million cell updates/sec

Title: US-09-979-558a-1\_COPY\_458\_476

Perfect score: 19

Sequence: 1 cccgggacgatgacatta 19

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 5615251 seqs, 3030001701 residues

Total number of hits satisfying chosen parameters: 11230502

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:\*\*

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- 3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq.\*
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- 9: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq.\*
- 10: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq.\*
- 11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq.\*
- 12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq.\*
- 13: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq.\*
- 14: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq.\*
- 15: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq.\*
- 16: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq.\*
- 17: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq.\*
- 18: /cgn2\_6/ptodata/1/pubpna/US10F\_PUBCOMB.seq.\*
- 19: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq.\*
- 20: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq.\*
- 21: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq.\*
- 22: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	16.4	86.3	1329	17	US-10-169-395-18
C 2	16.4	86.3	1882	9	US-09-925-298-301
C 3	16.4	86.3	1882	14	US-10-102-806-301
C 4	16.4	86.3	1926	9	US-09-764-853-238
C 5	16.4	86.3	1987	9	US-09-818-143-20
C 6	16.4	86.3	1989	10	US-09-946-374-76
C 7	16.4	86.3	1989	14	US-10-006-856A-76
C 8	16.4	86.3	1989	14	US-10-006-818A-76
C 9	16.4	86.3	1989	14	US-10-006-485A-76
C 10	16.4	86.3	1989	14	US-10-013-907A-76
C 11	16.4	86.3	1989	14	US-10-015-499A-76

C 12	16.4	86.3	1989	14	US-10-015-393A-76	Sequence 76, Appl
C 13	16.4	86.3	1989	14	US-10-015-869A-76	Sequence 76, Appl
C 14	16.4	86.3	1989	14	US-10-012-121A-76	Sequence 76, Appl
C 15	16.4	86.3	1989	14	US-10-006-116A-76	Sequence 76, Appl
C 16	16.4	86.3	1989	14	US-10-006-117A-76	Sequence 76, Appl
C 17	16.4	86.3	1989	14	US-10-017-527A-76	Sequence 76, Appl
C 18	16.4	86.3	1989	14	US-10-013-913A-76	Sequence 76, Appl
C 19	16.4	86.3	1989	14	US-10-007-194A-76	Sequence 76, Appl
C 20	16.4	86.3	1989	14	US-10-013-430A-76	Sequence 76, Appl
C 21	16.4	86.3	1989	14	US-10-011-671A-76	Sequence 76, Appl
C 22	16.4	86.3	1989	14	US-10-012-755A-76	Sequence 76, Appl
C 23	16.4	86.3	1989	14	US-10-015-386A-76	Sequence 76, Appl
C 24	16.4	86.3	1989	15	US-10-011-692A-76	Sequence 76, Appl
C 25	16.4	86.3	1989	15	US-10-006-768A-76	Sequence 76, Appl
C 26	16.4	86.3	1989	15	US-10-017-610A-76	Sequence 76, Appl
C 27	16.4	86.3	1989	15	US-10-006-063A-76	Sequence 76, Appl
C 28	16.4	86.3	1989	15	US-10-020-063A-76	Sequence 76, Appl
C 29	16.4	86.3	1989	15	US-10-015-391A-76	Sequence 76, Appl
C 30	16.4	86.3	1989	15	US-10-017-407A-76	Sequence 76, Appl
C 31	16.4	86.3	1989	15	US-10-011-833A-76	Sequence 76, Appl
C 32	16.4	86.3	1989	15	US-10-006-041A-76	Sequence 76, Appl
C 33	16.4	86.3	1989	15	US-10-015-822A-76	Sequence 76, Appl
C 34	16.4	86.3	1989	15	US-10-015-387A-76	Sequence 76, Appl
C 35	16.4	86.3	1989	15	US-10-006-130A-76	Sequence 76, Appl
C 36	16.4	86.3	1989	16	US-10-006-172A-76	Sequence 76, Appl
C 37	16.4	86.3	1989	16	US-10-017-253A-76	Sequence 76, Appl
C 38	16.4	86.3	1989	16	US-10-015-392A-76	Sequence 76, Appl
C 39	16.4	86.3	1989	16	US-10-017-306A-76	Sequence 76, Appl
C 40	16.4	86.3	1989	16	US-10-017-867A-76	Sequence 76, Appl
C 41	16.4	86.3	1989	16	US-10-012-064A-76	Sequence 76, Appl
C 42	16.4	86.3	1989	16	US-10-013-909A-76	Sequence 76, Appl
C 43	16.4	86.3	1989	16	US-10-015-671A-76	Sequence 76, Appl
C 44	16.4	86.3	1989	16	US-10-015-610A-76	Sequence 76, Appl
C 45	16.4	86.3	1989	16	US-10-012-137A-76	Sequence 76, Appl

#### ALIGNMENTS

RESULT 1  
US-10-169-395-18/c  
; Sequence 18, Application US/10169395  
; Publication No. US20040034192A1  
; GENERAL INFORMATION:  
; APPLICANT: KATO, Seishi  
; APPLICANT: KIMURA, Tomoko  
; TITLE OF INVENTION: HUMAN PROTEINS HAVING HYDROPHOBIC DOMAINS AND DNAB ENCODING  
; TITLE OF INVENTION: THESE PROTEINS  
; FILE REFERENCE: 01997.015100.US  
; CURRENT APPLICATION NUMBER: US/10/169,395  
; CURRENT FILING DATE: 2002-11-29  
; PRIOR APPLICATION NUMBER: JP 2000-585  
; PRIOR FILING DATE: 2000-01-06  
; PRIOR APPLICATION NUMBER: JP 2000-588  
; PRIOR FILING DATE: 2000-01-06  
; PRIOR APPLICATION NUMBER: JP 2000-2299  
; PRIOR FILING DATE: 2000-01-11  
; PRIOR APPLICATION NUMBER: JP 2000-26862  
; PRIOR FILING DATE: 2000-02-03  
; PRIOR APPLICATION NUMBER: JP 2000-58367  
; PRIOR FILING DATE: 2000-03-03  
; PRIOR APPLICATION NUMBER: PCT/JP00/09359  
; PRIOR FILING DATE: 2000-12-28  
; NUMBER OF SEQ ID NOS: 150  
; SEQ ID NO 18  
; LENGTH: 1329  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-169-395-18

Query Match 86.3%; Score 16.4; DB 17; Length 1329;  
Best Local Similarity 94.4%; Pred. No. 1.4e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCGGGGACGATGACATT 18  
 | | | | | | | | | | | | | | | | | |  
 Db 999 CTCGGGGACGATGACATT 982

## RESULT 2

US-09-925-298-301/c  
 ; Sequence 301, Application US/09925298  
 ; Publication No. US20020039764A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rosen et al.  
 ; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
 ; FILE REFERENCE: PA103  
 ; CURRENT APPLICATION NUMBER: US/09/925,298  
 ; CURRENT FILING DATE: 2001-08-10  
 ; PRIOR APPLICATION NUMBER: PCT/US00/05881  
 ; PRIOR FILING DATE: 2000-03-08  
 ; PRIOR APPLICATION NUMBER: 60/124,270  
 ; PRIOR FILING DATE: 1999-03-12  
 ; NUMBER OF SEQ ID NOS: 846  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 301  
 ; LENGTH: 1882  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: misc feature  
 ; LOCATION: (22)  
 ; OTHER INFORMATION: n equals a,t,g, or c  
 ; NAME/KEY: misc feature  
 ; LOCATION: (223)  
 ; OTHER INFORMATION: n equals a,t,g, or c  
 ; NAME/KEY: misc feature  
 ; LOCATION: (1840)  
 ; OTHER INFORMATION: n equals a,t,g, or c  
 ; NAME/KEY: misc feature  
 ; LOCATION: (1843)  
 ; OTHER INFORMATION: n equals a,t,g, or c  
 ; OTHER INFORMATION: n equals a,t,g, or c  
 ; US-09-925-298-301

Query Match 86.3%; Score 16.4; DB 9; Length 1882;  
 Best Local Similarity 94.4%; Pred. No. 1.4e+02;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCGGGGACGATGACATT 18  
 | | | | | | | | | | | | | | | | | |  
 Db 546 CTCGGGGACGATGACATT 529

## RESULT 3

US-10-102-806-301/c  
 ; Sequence 301, Application US/10102806  
 ; Publication No. US20030054421A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rosen et al.  
 ; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
 ; FILE REFERENCE: PA103P1C1  
 ; CURRENT APPLICATION NUMBER: US/10/102,806  
 ; CURRENT FILING DATE: 2002-03-22  
 ; PRIOR APPLICATION NUMBER: 09/925,298  
 ; PRIOR FILING DATE: 2001-08-10  
 ; PRIOR APPLICATION NUMBER: PCT/US00/05881  
 ; PRIOR FILING DATE: 2000-03-08  
 ; PRIOR APPLICATION NUMBER: 60/124,270  
 ; PRIOR FILING DATE: 1999-03-12  
 ; NUMBER OF SEQ ID NOS: 846  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 301  
 ; LENGTH: 1882  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:

; NAME/KEY: misc feature  
 ; LOCATION: (22)  
 ; OTHER INFORMATION: n equals a,t,g, or c  
 ; NAME/KEY: misc feature  
 ; LOCATION: (223)  
 ; OTHER INFORMATION: n equals a,t,g, or c  
 ; NAME/KEY: misc feature  
 ; LOCATION: (1840)  
 ; OTHER INFORMATION: n equals a,t,g, or c  
 ; NAME/KEY: misc feature  
 ; LOCATION: (1849)  
 ; OTHER INFORMATION: n equals a,t,g, or c  
 ; US-10-102-806-301

Query Match 86.3%; Score 16.4; DB 14; Length 1882;  
 Best Local Similarity 94.4%; Pred. No. 1.4e+02;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCGGGGACGATGACATT 18  
 | | | | | | | | | | | | | | | | | |  
 Db 546 CTCGGGGACGATGACATT 529

## RESULT 4

US-09-764-853-238/c  
 ; Sequence 238, Application US/09764853  
 ; Patent No. US20020090672A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rosen et al.  
 ; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
 ; FILE REFERENCE: PJZ06  
 ; CURRENT APPLICATION NUMBER: US/09/764,853  
 ; CURRENT FILING DATE: 2001-01-17  
 ; Prior application data removed - consult PALM or file wrapper  
 ; NUMBER OF SEQ ID NOS: 939  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 238  
 ; LENGTH: 1926  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; US-09-764-853-238

Query Match 86.3%; Score 16.4; DB 9; Length 1926;  
 Best Local Similarity 94.4%; Pred. No. 1.4e+02;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCGGGGACGATGACATT 18  
 | | | | | | | | | | | | | | | | | |  
 Db 590 CTCGGGGACGATGACATT 573

## RESULT 5

US-09-818-143-20/c  
 ; Sequence 20, Application US/09818143  
 ; Patent No. US20020019000A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Walker, Michael G.  
 ; APPLICANT: Volkmut, Wayne  
 ; APPLICANT: Klingler, Tod M.  
 ; TITLE OF INVENTION: POLYNUCLEOTIDES COEXPRESSED WITH MATRIX-REMODELING GENES  
 ; FILE REFERENCE: PB-0004 CIP  
 ; CURRENT APPLICATION NUMBER: US/09/818,143  
 ; CURRENT FILING DATE: 2001-03-26  
 ; NUMBER OF SEQ ID NOS: 23  
 ; SOFTWARE: PERL Program  
 ; SEQ ID NO 20  
 ; LENGTH: 1987  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; OTHER INFORMATION: 3948614CB1  
 ; US-09-818-143-20

Query Match 86.3%; Score 16.4; DB 9; Length 1987;  
Best Local Similarity 94.4%; Pred. No. 1.4e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCGGGGACGATGACATT 18  
DB 733 CTCGGGACGATGACATT 716

## RESULT 6

US-09-946-374-76/c

; Sequence 76, Application US/09946374

; Publication No. US20030073129A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, Christopher J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth J.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Smith, Victoria

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; TITLE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: P2830P1C1

; CURRENT APPLICATION NUMBER: US/09/946,374

; CURRENT FILING DATE: 2001-09-04

; PRIOR APPLICATION NUMBER: 60/098716

; PRIOR FILING DATE: 1998-09-01

; PRIOR APPLICATION NUMBER: 60/098723

; PRIOR FILING DATE: 1998-09-01

; PRIOR APPLICATION NUMBER: 60/098749

; PRIOR FILING DATE: 1998-09-01

; PRIOR APPLICATION NUMBER: 60/098750

; PRIOR FILING DATE: 1998-09-01

; PRIOR APPLICATION NUMBER: 60/098803

; PRIOR FILING DATE: 1998-09-02

; PRIOR APPLICATION NUMBER: 60/098821

; PRIOR FILING DATE: 1998-09-02

; PRIOR APPLICATION NUMBER: 60/098843

; PRIOR FILING DATE: 1998-09-02

; PRIOR APPLICATION NUMBER: 60/099536

; PRIOR FILING DATE: 1998-09-09

; PRIOR APPLICATION NUMBER: 60/099596

; PRIOR FILING DATE: 1998-09-09

; PRIOR APPLICATION NUMBER: 60/099598

; PRIOR FILING DATE: 1998-09-09

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; PRIOR FILING DATE: 1998-09-09

; PRIOR APPLICATION NUMBER: 60/099642

; PRIOR FILING DATE: 1998-09-09

; PRIOR APPLICATION NUMBER: 60/099741

; PRIOR FILING DATE: 1998-09-10

; PRIOR APPLICATION NUMBER: 60/099754

; PRIOR FILING DATE: 1998-09-10

; PRIOR APPLICATION NUMBER: 60/099763

; PRIOR FILING DATE: 1998-09-10

; PRIOR APPLICATION NUMBER: 60/099792

; PRIOR FILING DATE: 1998-09-10

; PRIOR APPLICATION NUMBER: 60/099808

; PRIOR FILING DATE: 1998-09-10

; PRIOR FILING DATE: 1998-09-10  
; PRIOR APPLICATION NUMBER: 60/099812  
; PRIOR FILING DATE: 1998-09-10  
; PRIOR APPLICATION NUMBER: 60/099815  
; PRIOR FILING DATE: 1998-09-10  
; PRIOR APPLICATION NUMBER: 60/099816  
; PRIOR FILING DATE: 1998-09-10  
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; PRIOR FILING DATE: 1998-09-15  
; PRIOR APPLICATION NUMBER: 60/100388  
; PRIOR FILING DATE: 1998-09-15  
; PRIOR APPLICATION NUMBER: 60/100390  
; PRIOR FILING DATE: 1998-09-15  
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; PRIOR FILING DATE: 1998-09-16  
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; PRIOR FILING DATE: 1998-09-16  
; PRIOR APPLICATION NUMBER: 60/100661  
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; PRIOR FILING DATE: 1998-09-17  
; PRIOR APPLICATION NUMBER: 60/101014  
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; PRIOR FILING DATE: 1998-09-22  
; PRIOR APPLICATION NUMBER: 60/101471  
; PRIOR FILING DATE: 1998-09-23  
; PRIOR APPLICATION NUMBER: 60/101472  
; PRIOR FILING DATE: 1998-09-23  
; PRIOR APPLICATION NUMBER: 60/101474  
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; PRIOR APPLICATION NUMBER: 60/101477  
; PRIOR FILING DATE: 1998-09-23  
; PRIOR APPLICATION NUMBER: 60/101479  
; PRIOR FILING DATE: 1998-09-23  
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; PRIOR APPLICATION NUMBER: 60/101741  
; PRIOR FILING DATE: 1998-09-24  
; PRIOR APPLICATION NUMBER: 60/101743  
; PRIOR FILING DATE: 1998-09-24  
; PRIOR APPLICATION NUMBER: 60/101915  
; PRIOR FILING DATE: 1998-09-24  
; PRIOR APPLICATION NUMBER: 60/101916  
; PRIOR FILING DATE: 1998-09-24  
; PRIOR APPLICATION NUMBER: 60/102207  
; PRIOR FILING DATE: 1998-09-29

Query Match	86.3%	Score 16.4;	DB 10;	Length 1989;
Best Local Similarity	94.4%;	Pred. No. 1.4e+00;		
Matches 17;	Conservative	0;	Mismatches 1;	Indels 0;
Gaps 0;				
QY	1	CCCGGGGACGATGACATT	18	
Db	732	CTCGGGGACGATGACATT	715	

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Query Match      86.3%; Score 16.4; DB 14; Length 1989;
Best Local Similarity 94.4%; Pred. NO. 1.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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RESULT 8
US-10-006-818A-76/c
; Sequence 76, Application US/10006818A
; Publication No. US20030054406A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Iuc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830PIC4
; CURRENT APPLICATION NUMBER: US/10/006,818A
; CURRENT FILING DATE: 2001-12-06
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 76
; LENGTH: 1989
; TYPE: DNA
; ORGANISM: Homo sapiens

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;; PRIOR FILING DATE: 1998-09-29  
;; PRIOR APPLICATION NUMBER: 60/102331  
;; PRIOR FILING DATE: 1998-09-29  
;; PRIOR APPLICATION NUMBER: 60/102484  
;; PRIOR FILING DATE: 1998-09-30  
;; PRIOR APPLICATION NUMBER: 60/102487  
;; PRIOR FILING DATE: 1998-09-30  
;; PRIOR APPLICATION NUMBER: 60/102570  
;; PRIOR FILING DATE: 1998-09-30  
;; PRIOR APPLICATION NUMBER: 60/102571  
;; PRIOR FILING DATE: 1998-09-30  
;; PRIOR APPLICATION NUMBER: 60/102684  
;; PRIOR FILING DATE: 1998-10-01  
;; PRIOR APPLICATION NUMBER: 60/102687  
;; PRIOR FILING DATE: 1998-10-01  
;; PRIOR APPLICATION NUMBER: 60/102965  
;; PRIOR FILING DATE: 1998-10-02  
;; PRIOR APPLICATION NUMBER: 60/103258  
;; PRIOR FILING DATE: 1998-10-06  
;; PRIOR APPLICATION NUMBER: 60/103314  
;; PRIOR FILING DATE: 1998-10-07  
;; PRIOR APPLICATION NUMBER: 60/103315  
;; PRIOR FILING DATE: 1998-10-07  
;; PRIOR APPLICATION NUMBER: 60/103328  
;; PRIOR FILING DATE: 1998-10-07  
;; PRIOR APPLICATION NUMBER: 60/103395  
;; PRIOR FILING DATE: 1998-10-07  
;; PRIOR APPLICATION NUMBER: 60/103396  
;; PRIOR FILING DATE: 1998-10-07  
;; PRIOR APPLICATION NUMBER: 60/103401  
;; PRIOR FILING DATE: 1998-10-07  
;; PRIOR APPLICATION NUMBER: 60/103449  
;; PRIOR FILING DATE: 1998-10-06  
;; PRIOR APPLICATION NUMBER: 60/103633  
;; PRIOR FILING DATE: 1998-10-08  
;; PRIOR APPLICATION NUMBER: 60/103678  
;; PRIOR FILING DATE: 1998-10-08  
;; PRIOR APPLICATION NUMBER: 60/103679  
;; PRIOR FILING DATE: 1998-10-08  
;; PRIOR APPLICATION NUMBER: 60/103711  
;; PRIOR FILING DATE: 1998-10-08  
;; PRIOR APPLICATION NUMBER: 60/104257  
;; PRIOR FILING DATE: 1998-10-14  
;; PRIOR APPLICATION NUMBER: 60/104987  
;; PRIOR FILING DATE: 1998-10-20  
;; PRIOR APPLICATION NUMBER: 60/105000  
;; PRIOR FILING DATE: 1998-10-20  
;; PRIOR APPLICATION NUMBER: 60/105002  
;; PRIOR FILING DATE: 1998-10-20  
;; PRIOR APPLICATION NUMBER: 60/105104  
;; PRIOR FILING DATE: 1998-10-21  
;; PRIOR APPLICATION NUMBER: 60/105169  
;; PRIOR FILING DATE: 1998-10-22  
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;; PRIOR FILING DATE: 1998-10-22  
;; PRIOR APPLICATION NUMBER: 60/105693  
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;; PRIOR APPLICATION NUMBER: 60/105807  
;; PRIOR FILING DATE: 1998-10-27  
;; PRIOR APPLICATION NUMBER: 60/105881  
;; PRIOR FILING DATE: 1998-10-27  
;; PRIOR APPLICATION NUMBER: 60/105882  
;; PRIOR FILING DATE: 1998-10-27  
;; PRIOR APPLICATION NUMBER: 60/106023  
;; PRIOR FILING DATE: 1998-10-28

Query Match 86.3%; Score 16.4; DB 14; Length 1989;  
Best Local Similarity 94.4%; Pred. No. 1.4e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCCGGGACGATGACATT 18

Db 732 CTCGGGACGATGACATT 715

RESULT 10

US-10-013-907A-76/c  
; Sequence 76, Application US/10013907A  
; Publication No. US20030064925A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan I.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2830PIC34  
; CURRENT APPLICATION NUMBER: US/10/013,907A  
; CURRENT FILING DATE: 2001-12-10  
; Prior Application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 477  
; SEQ ID NO 76  
; LENGTH: 1989  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-013-907A-76

Query Match 86.3%; Score 16.4; DB 14; Length 1989;  
Best Local Similarity 94.4%; Pred. No. 1.4e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCCGGGACGATGACATT 18  
Db 732 CTCGGGACGATGACATT 715

RESULT 11

US-10-015-499A-76/c  
; Sequence 76, Application US/10015499A  
; Publication No. US20030065142A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan I.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2830PIC42  
; CURRENT APPLICATION NUMBER: US/10/015,499A  
; CURRENT FILING DATE: 2001-12-11  
; Prior Application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 477  
; SEQ ID NO 76  
; LENGTH: 1989

; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-015-499A-76

Query Match 86.3%; Score 16.4; DB 14; Length 1989;  
Best Local Similarity 94.4%; Pred. No. 1.4e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCGGGGACGATGACATT 18  
| | | | | | | | | | | | | | | | | | | | | |  
Db 732 CTCGGGGACGATGACATT 715

## RESULT 12

US-10-015-393A-76/c  
; Sequence 76, Application US/10015393A  
; Publication No. US20030069179A1  
; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnovers, Luc  
; APPLICANT: Eaton, Dan I.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2830PIC46  
; CURRENT APPLICATION NUMBER: US/10/015,393A  
; CURRENT FILING DATE: 2002-06-10  
; Prior Application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 477  
; SEQ ID NO 76

; LENGTH: 1989  
; TYPE: DNA

; ORGANISM: Homo sapiens  
US-10-015-393A-76

Query Match 86.3%; Score 16.4; DB 14; Length 1989;  
Best Local Similarity 94.4%; Pred. No. 1.4e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCGGGGACGATGACATT 18  
| | | | | | | | | | | | | | | | | | | | | |  
Db 732 CTCGGGGACGATGACATT 715

## RESULT 13

US-10-015-869A-76/c  
; Sequence 76, Application US/10015869A  
; Publication No. US20030073130A1  
; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnovers, Luc  
; APPLICANT: Eaton, Dan I.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2830PIC45  
; CURRENT APPLICATION NUMBER: US/10/015,869A  
; CURRENT FILING DATE: 2002-06-25  
; Prior Application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 477  
; SEQ ID NO 76

; LENGTH: 1989  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-015-869A-76

Query Match 86.3%; Score 16.4; DB 14; Length 1989;  
Best Local Similarity 94.4%; Pred. No. 1.4e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCGGGGACGATGACATT 18  
| | | | | | | | | | | | | | | | | | | | | |  
Db 732 CTCGGGGACGATGACATT 715

## RESULT 14

US-10-012-121A-76/c  
; Sequence 76, Application US/10012121A  
; Publication No. US20030073810A1  
; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnovers, Luc  
; APPLICANT: Eaton, Dan I.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2830PIC20  
; CURRENT APPLICATION NUMBER: US/10/012,121A  
; CURRENT FILING DATE: 2001-12-07  
; Prior Application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 477  
; SEQ ID NO 76

; LENGTH: 1989  
; TYPE: DNA

; ORGANISM: Homo sapiens  
US-10-012-121A-76

Query Match 86.3%; Score 16.4; DB 14; Length 1989;  
Best Local Similarity 94.4%; Pred. No. 1.4e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCGGGGACGATGACATT 18  
| | | | | | | | | | | | | | | | | | | | | |  
Db 732 CTCGGGGACGATGACATT 715

## RESULT 15

US-10-006-116A-76/c  
; Sequence 76, Application US/10006116A  
; Publication No. US20030082626A1  
; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnovers, Luc  
; APPLICANT: Eaton, Dan I.  
; APPLICANT: Ferrara, Napoleone

APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2830P1C15  
CURRENT APPLICATION NUMBER: US/10/006.116A  
CURRENT FILING DATE: 2001-12-16  
PRIOR APPLICATION NUMBER: 60/098716  
PRIOR FILING DATE: 1998-09-01  
PRIOR APPLICATION NUMBER: 60/098723  
PRIOR FILING DATE: 1998-09-01  
PRIOR APPLICATION NUMBER: 60/098749  
PRIOR FILING DATE: 1998-09-01  
PRIOR APPLICATION NUMBER: 60/098750  
PRIOR FILING DATE: 1998-09-01  
PRIOR APPLICATION NUMBER: 60/098803  
PRIOR FILING DATE: 1998-09-02  
PRIOR APPLICATION NUMBER: 60/098821  
PRIOR FILING DATE: 1998-09-02  
PRIOR APPLICATION NUMBER: 60/098843  
PRIOR FILING DATE: 1998-09-02  
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PRIOR FILING DATE: 1998-09-30  
PRIOR APPLICATION NUMBER: 60/102571  
PRIOR FILING DATE: 1998-09-30  
PRIOR APPLICATION NUMBER: 60/102684  
PRIOR FILING DATE: 1998-10-01  
PRIOR APPLICATION NUMBER: 60/102687  
PRIOR FILING DATE: 1998-10-01  
PRIOR APPLICATION NUMBER: 60/102965  
PRIOR FILING DATE: 1998-10-02  
PRIOR APPLICATION NUMBER: 60/103258  
PRIOR FILING DATE: 1998-10-06  
PRIOR APPLICATION NUMBER: 60/103314  
PRIOR FILING DATE: 1998-10-07



;; PRIOR APPLICATION NUMBER: 60/103315  
;; PRIOR FILING DATE: 1998-10-07  
;; PRIOR APPLICATION NUMBER: 60/103328  
;; PRIOR FILING DATE: 1998-10-07  
;; PRIOR APPLICATION NUMBER: 60/103395  
;; PRIOR FILING DATE: 1998-10-07  
;; PRIOR APPLICATION NUMBER: 60/103396  
;; PRIOR FILING DATE: 1998-10-07  
;; PRIOR APPLICATION NUMBER: 60/103401  
;; PRIOR FILING DATE: 1998-10-07  
;; PRIOR APPLICATION NUMBER: 60/103449  
;; PRIOR FILING DATE: 1998-10-06  
;; PRIOR APPLICATION NUMBER: 60/103633  
;; PRIOR FILING DATE: 1998-10-08  
;; PRIOR APPLICATION NUMBER: 60/103678  
;; PRIOR FILING DATE: 1998-10-08  
;; PRIOR APPLICATION NUMBER: 60/103679  
;; PRIOR FILING DATE: 1998-10-08  
;; PRIOR APPLICATION NUMBER: 60/103711  
;; PRIOR FILING DATE: 1998-10-08  
;; PRIOR APPLICATION NUMBER: 60/104257  
;; PRIOR FILING DATE: 1998-10-14  
;; PRIOR APPLICATION NUMBER: 60/104987  
;; PRIOR FILING DATE: 1998-10-20  
;; PRIOR APPLICATION NUMBER: 60/105000  
;; PRIOR FILING DATE: 1998-10-20  
;; PRIOR APPLICATION NUMBER: 60/105002  
;; PRIOR FILING DATE: 1998-10-20  
;; PRIOR APPLICATION NUMBER: 60/105104  
;; PRIOR FILING DATE: 1998-10-21  
;; PRIOR APPLICATION NUMBER: 60/105169  
;; PRIOR FILING DATE: 1998-10-22  
;; PRIOR APPLICATION NUMBER: 60/105266  
;; PRIOR FILING DATE: 1998-10-22  
;; PRIOR APPLICATION NUMBER: 60/105693  
;; PRIOR FILING DATE: 1998-10-26  
;; PRIOR APPLICATION NUMBER: 60/105694  
;; PRIOR FILING DATE: 1998-10-26  
;; PRIOR APPLICATION NUMBER: 60/105807  
;; PRIOR FILING DATE: 1998-10-27  
;; PRIOR APPLICATION NUMBER: 60/105881  
;; PRIOR FILING DATE: 1998-10-27  
;; PRIOR APPLICATION NUMBER: 60/105882  
;; PRIOR FILING DATE: 1998-10-27  
;; PRIOR APPLICATION NUMBER: 60/106023  
;; PRIOR FILING DATE: 1998-10-28

Query Match 86.3%; Score 16.4; DB 14; Length 1989;  
Best Local Similarity 94.4%; Pred. No. 1.4e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCGGGACGATGACATT 18  
Db 732 CTCGGGGACGATGACATT 715

Search completed: April 12, 2005, 10:50:17  
Job time : 290 secs

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 12, 2005, 08:13:54 ; Search time 1738 Seconds  
(without alignments)  
416.123 Million cell updates/sec

Title: US-09-979-558a-1\_COPY\_458\_476

Perfect score: 19

Sequence: 1 cccgggacgatgacatta 19

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : EST:\*

1: gb\_est1:\*

2: gb\_est2:\*

3: gb\_hc:\*

4: gb\_est3:\*

5: gb\_est4:\*

6: gb\_est5:\*

7: gb\_est6:\*

8: gb\_ges1:\*

9: gb\_ges2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	17.4	91.6	695	9 AG416365	AG416365 Mus muscu
C 2	17.4	91.6	793	9 CR004289	CR004289 Forward s
C 3	16.4	86.3	337	7 W92952	W92952 z492e10.1
C 4	16.4	86.3	340	1 AA037563	AA037563 2k34a03.r
C 5	16.4	86.3	369	7 W45082	W45082 zc21g10.1
C 6	16.4	86.3	419	7 CN395703	CN395703 170004240
C 7	16.4	86.3	443	7 CN918724	CN918724 030207ABP
C 8	16.4	86.3	513	1 AA115144	AA115144 z110f09.r
C 9	16.4	86.3	531	7 CO610497	CO610497 DG8-94n3
C 10	16.4	86.3	533	1 A1817726	A1817726 wk25e07.x
C 11	16.4	86.3	537	7 W16559	W16559 zbl1b12.1
C 12	16.4	86.3	539	1 A1772402	A1772402 EST253502
C 13	16.4	86.3	554	4 B1627185	B1627185 RH68421.5
C 14	16.4	86.3	562	2 AW963853	AW963853 EST375926
C 15	16.4	86.3	594	7 CO598991	CO598991 DG8-174n1
C 16	16.4	86.3	595	2 BF342569	BF342569 602013893
C 17	16.4	86.3	682	4 BG127540	BG127540 EST473282
C 18	16.4	86.3	768	4 B1758715	B1758715 603024016
C 19	16.4	86.3	799	4 B1754114	B1754114 603027673
C 20	16.4	86.3	817	7 CO596974	CO596974 DG8-138n1
C 21	16.4	86.3	903	5 BQ881886	BQ881886 AGENCOURT
C 22	16.4	86.3	957	5 BQ177752	BQ177752 AGENCOURT
C 23	16.4	86.3	1008	5 BX439049	BX439049
C 24	16.4	86.3	1054	1 AL553402	AL553402 AL553402

C 25	16.4	86.3	1060	5 BUI34659	BUI34659 603121881
C 26	16.4	86.3	1129	5 BM924224	BM924224 AGENCOURT
C 27	16.4	86.3	1650	3 CF592046	CF592046 full-length
C 28	16.4	86.3	1987	2 AW888223	AW888223 MYRA8 Hum
C 29	16	84.2	373	6 CA269132	CA269132 SCURT306
C 30	16	84.2	435	1 A1329817	A1329817 b8f06ne.r
C 31	16	84.2	511	1 A1397616	A1397616 NCSC5C8T7
C 32	16	84.2	517	2 AW186852	AW186852 BNLGHI597
C 33	16	84.2	639	1 AV849197	AV849197 AV849197
C 34	16	84.2	648	1 A1398536	A1398536 NCM07A977
C 35	16	84.2	686	1 AV849138	AV849138 AV849138
C 36	16	84.2	701	8 BH954585	BH954585 odi78c12.
C 37	16	84.2	709	8 BH954543	BH954543 odi78b12.
C 38	16	84.2	831	8 BH423226	BH423226 BOHSZ48TR
C 39	16	84.2	3342	9 CL982185	CL982185 OeIFSC046
C 40	15.8	83.2	192	8 BZ672389	BZ672389 PUBEN327D
C 41	15.8	83.2	215	1 AV025145	AV025145 AV025145
C 42	15.8	83.2	237	5 BF105595	BF105595 BF105595
C 43	15.8	83.2	243	4 BM106925	BM106925 511009 MA
C 44	15.8	83.2	269	7 CF613570	CF613570 CES008156
C 45	15.8	83.2	289	5 BQ640964	BQ640964 SSH-Bbblic

#### ALIGNMENTS

RESULT 1	AG416365	695 bp	DNA	linear	GSS 03-JUN-2004
LOCUS	Mus musculus molossinus DNA, clone:MSMg01-278N11.T7, genomic survey				
DEFINITION	sequence.				
ACCESSION	AG416365				
VERSION	AG416365.1	GI:48059339			
KEYWORDS	GSS.				
SOURCE	Mus musculus molossinus				
ORGANISM	Mus musculus molossinus				
REFERENCE	1				
AUTHORS	Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.				
TITLE	BAC end Sequences of Library MSMg01				
JOURNAL	Unpublished				
REFERENCE	2 (bases 1 to 695)				
AUTHORS	Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.				
TITLE	Direct Submission				
JOURNAL	Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); Japan 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: hattori@psc.riken.jp, URL: http://hgp.gsc.riken.go.jp/, Tel: 81-45-503-9111, Fax: 81-45-503-9170)				
COMMENT	Clones are derived from the mouse BAC library MSMg01. For BAC library availability, please contact Kuniya Abe (abe@rtc.riken.jp). Tsukuba Institute of Physical and Chemical Research, The Institute of Physical and Chemical Research (RIKEN) 3-1-1 Koyadai, Tsukuba, 305-0074 Japan phone: 81-298-36-9189, fax: 81-298-36-9199 e-mail: abe@rtc.riken.jp PRIMERS Sequencing : T7 LIBRARY Vector : pBACE3.6 R.Site 1 : EcoRI. R.Site 2 : EcoRI. Location/Qualifiers 1. .695 /organism="Mus musculus molossinus" /mol_type="genomic DNA" /sub_species="molossinus" /db_xref="taxon:57486" /clone="MSMg01-278N11.T7" /sex="male" /tissue_type="mixture of kidney and spleen" /clone_lib="MSMg01 Mouse Male BAC Library"				



Insert Length: 597 Std Error: 0.00  
Seq primer: -28M13 rev2 from Amersham  
High quality sequence stop: 121.

## FEATURES

## source

```
1..340
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:3758398"
/db_xref="taxon:9606"
/clone="IMAGE:484684"
/sex="female"
/dev_stages="adult"
/lab_host="DH10B"
/clone_lib="Soares pregnant uterus NhPU"
/notes="Organ: uterus; Vector: pT7T3-Pac; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5, AACTGGAAGATTCGGCGCCGCTTTTCTTTTCTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library constructed by M. Fatima Bonaldo."
```

## ORIGIN

```
Query Match      86.3%; Score 16.4; DB 1; Length 340;
Best Local Similarity 94.4%; Pred. No. 1e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 1 CCCGGGACGATGACATT 18
    |||||
Db 18 CTCGGGACGATGACATT 35
```

## RESULT 5

## W45082/c

## LOCUS

```
DEFINITION      W45082 369 bp mRNA linear EST 10-OCT-1996
                  clone IMAGE:323010 5', mRNA sequence.
```

## ACCESSION

## W45082

## VERSION

## W45082.1

## KEYWORDS

## EST.

## SOURCE

## Homo sapiens

## ORGANISM

## Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

## Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## 1 (bases 1 to 369)

## Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevas, K., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R.

## The WashU-Merck EST Project

## Unpublished (1995)

## Contact: Wilson RK

## Washington University School of Medicine

## 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

## Tel: 314 286 1800

## Fax: 314 286 1810

## Email: est@wustl.edu

## This clone is available royalty-free through LNL; contact the

## IMAGE Consortium (info@image.llnl.gov) for further information.

## Insert Length: 1423 Std Error: 0.00

## Seq primer: mob.REGA+ET

## High quality sequence stop: 326.

## Location/Qualifiers

## 1..369

## /organism="Homo sapiens"

## /mol\_type="mRNA"

## /db\_xref="GDB:1254522"

## /db\_xref="taxon:9606"

## /clone="IMAGE:323010"

## /tissue\_type="senescent fibroblast"

## FEATURES

## source

```
1..369
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:1254522"
/db_xref="taxon:9606"
/clone="IMAGE:323010"
/tissue_type="senescent fibroblast"
```

```
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares senescent fibroblasts NhHSF"
/notes="Vector: pT7T3D (Pharmacia) with a modified
polylinker V type: phagemid; Site 1: Not I; Site 2: Eco
RI; 1st strand cDNA was primed with a Not I - oligo(dT)
primer [5, TGTACCAATCTGAAGTGGGAGCGCGCATTTTTTTTTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT7T3 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by Bento
Soares and M. Fatima Bonaldo."
```

## ORIGIN

```
Query Match      86.3%; Score 16.4; DB 7; Length 369;
Best Local Similarity 94.4%; Pred. No. 1e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 1 CCCGGGACGATGACATT 18
    |||||
Db 158 CTCGGGACGATGACATT 141
```

## RESULT 6

## CN395703/c

## LOCUS

```
DEFINITION      CN395703 419 bp mRNA linear EST 16-MAY-2004
                  17000424021755 GRN_ES Homo sapiens cDNA 5', mRNA sequence.
```

## ACCESSION

## CN395703

## VERSION

## CN395703.1

## KEYWORDS

## EST.

## SOURCE

## Homo sapiens

## ORGANISM

## Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

## Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## 1 (bases 1 to 419)

## Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Flisk, G.J., Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R., Lebkowski, J. and Stanton, L.W.

## Transcriptome characterization elucidates signaling networks that

## control human ES cell growth and differentiation

## Nat. Biotechnol. 22 (6), 707-716 (2004)

## Contact: Brandenberger R

## Regenerative Medicine

## Gen Corporation

## 230 Constitution Drive, Menlo Park, CA 94025, USA

## Tel: 650 473 8658

## Fax: 650 473 7760

## Email: rbrandenberger@gen.com

## Insert Length: 419 Std Error: 0.00.

## Location/Qualifiers

## 1..419

## /organism="Homo sapiens"

## /mol\_type="mRNA"

## /db\_xref="taxon:9606"

## /tissue\_type="embryonic stem cells, cell lines H1, H7, and H9"

## /clone\_lib="GRN ES"

## /notes="oligo dT primed, full-length enriched cDNA library

## from undifferentiated hES cell lines H1 (p32), H7 (p29),

## and H9 (p26) maintained in feeder-free conditions"

## ORIGIN

```
Query Match      86.3%; Score 16.4; DB 7; Length 419;
Best Local Similarity 94.4%; Pred. No. 1e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 1 CCCGGGACGATGACATT 18
    |||||
Db 163 CTCGGGACGATGACATT 146
```

## RESULT 7

```

CN918724
LOCUS      CN918724      443 bp      mRNA      linear      EST 07-JUN-2004
DEFINITION 030207ABPB006067HT (ABPB) M9 root tips Malus x domestica cDNA clone
ABPB006067, mRNA sequence.
ACCESSION  CN918724
VERSION     CN918724.1 GI:48391537
KEYWORDS    EST.
SOURCE      Malus x domestica (cultivated apple)
ORGANISM    Malus x domestica
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids I; Rosales; Rosaceae; Maloideae; Malus.
REFERENCE   1 (bases 1 to 443)
AUTHORS    Beuning, L., Bowen, J., Crowhurst, R., Gleave, A., Janssen, B.,
            McCartney, S., Newcomb, R., Ross, G., Snowden, K., Walton, E. and Yauk, Y.
TITLE      HortResearch Apple EST Project
JOURNAL     Unpublished (2004)
COMMENT     Contact: Gleave, A.
            Sequencing Facility
            The Horticulture and Food Research Institute of New Zealand Ltd
            120 Mt Albert Rd, Mt Albert, Auckland, New Zealand
            Tel: 00 64 09 815 4200
            Fax: 00 64 09 815 4201
            Email: est@hortresearch.co.nz.
FEATURES   source
            Location/Qualifiers
            1..443
               /organism="Malus x domestica"
               /mol_type="mRNA"
               /db_xref="taxon:3750"
               /clone="ABPB006067"
               /tissue_type="Root tips (distal 1.5 cm)"
               /clone_lib="(ABPB) M9 root tips"
               /note="vector: phuescript SK(-); Library sequenced by
               Genesis Research & Development"
ORIGIN
Query Match      86.3%; Score 16.4; DB 7; Length 443;
Best Local Similarity 94.4%; Pred. No. 1e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCGGGGACGATGACATT 18
    |||||
Db 392 CCGGGGACGATGACTT 409

RESULT 8
AA115144
LOCUS      AA115144      513 bp      mRNA      linear      EST 15-NOV-1996
DEFINITION z110f09.t1 Soares_pregnant uterus_NBHPU Homo sapiens cDNA clone
IMAGE:501545 5', mRNA sequence.
ACCESSION  AA115144
VERSION     AA115144.1 GI:1670568
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 513)
AUTHORS    Hallier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
            Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
            Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
            Trevaaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and
            Wilson, R.
TITLE      The WashU-Merck EST Project
JOURNAL     Unpublished (1995)
COMMENT     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@wustl.edu
            This clone is available royalty-free through LLNL; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.

```

```

Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 392.
Location/Qualifiers
1..513
   /organism="Homo sapiens"
   /mol_type="mRNA"
   /db_xref="GDB:3806533"
   /db_xref="taxon:9606"
   /clone="IMAGE:501545"
   /sex="female"
   /dev_stage="adult"
   /lab_host="DH10B"
   /clone_lib="Soares_pregnant uterus_NBHPU"
   /note="Organ: uterus; Vector: pTV3-Pac; Site 1: Not I;
   Site 2: Eco RI; 1st strand cDNA was primed with a Not I -
   oligo(dT) primer [5',
   AACTGGAAGATTCCGGCGCCCTTTTCTTTT 3'],
   double-stranded cDNA was ligated to Eco RI adaptors
   (Pharmacia), digested with Not I and cloned into the Not I
   and Eco RI sites of the modified pTV3 vector. Library
   went through one round of normalization. Library
   constructed by M. Fatima Bonaldo."
ORIGIN
Query Match      86.3%; Score 16.4; DB 1; Length 513;
Best Local Similarity 94.4%; Pred. No. 1e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCGGGGACGATGACATT 18
    |||||
Db 18 CTCGGGACGATGACATT 35

RESULT 9
CO610497/c
LOCUS      CO610497      531 bp      mRNA      linear      EST 21-JUL-2004
DEFINITION DG8-94n3 DG8-testis Canis familiaris cDNA 3', mRNA sequence.
ACCESSION  CO610497
VERSION     CO610497.1 GI:50456061
KEYWORDS    EST.
SOURCE      Canis familiaris (dog)
ORGANISM    Canis familiaris
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE   1 (bases 1 to 531)
AUTHORS    Schluter, T., Hermanns, J., Weindel, M., Schuette, D., Kranz, H.,
            Henrich, J. and Loebbert, R.
TITLE      Dog arrayTAG cDNA clone collection
JOURNAL     Unpublished (2004)
COMMENT     Contact: Thomas Schluter
            LION bioscience AG
            Walhoferstrasse 98, D-69123 Heidelberg, Germany
            Tel: +49 6221 4038 150
            Fax: +49 6221 4038 290
            Email: Thomas.Schluter@lionbioscience.com.
FEATURES   source
            Location/Qualifiers
            1..531
               /organism="Canis familiaris"
               /mol_type="mRNA"
               /strain="Beagle"
               /db_xref="taxon:9615"
               /tissue_type="testis"
               /dev_stage="adult"
               /lab_host="DH10B"
               /clone_lib="DG8-testis"
               /note="Organ: testis; Vector: Dog phuescript LION"
ORIGIN
Query Match      86.3%; Score 16.4; DB 7; Length 531;
Best Local Similarity 94.4%; Pred. No. 1e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CCGGGGACGATGACATTA 19

```



TITLE Giovannoni, J.J. and Martin, G.B.  
 JOURNAL Generation of ESTs from *Pseudomonas* resistant tomato  
 COMMENT Unpublished (1999)  
 Contact: CUGI  
 Clemson University Genomics Institute  
 100 Jordan Hall, Clemson, SC 29634, USA  
 Email: <http://www.genome.clemson.edu/orders/index.html>  
 5 prime sequence.

## FEATURES

Location/Qualifiers

1..539

/organism="Lycopersicon esculentum"

/mol\_type="mRNA"

/cultivar="Ril-12 (35S::Pto in Rio Grande x Money Maker)"

/db\_xref="taxon:4081"

/clone="cLER2H9"

/tissue\_type="leaf"

/dev\_stage="4-week old"

/lab\_host="SOLR"

/clone\_lib="tomato resistant, Cornell"

/note="vector: pBluescript SK(-); Site 1: EcoRI; Site 2:

XhoI; cLER - Tomato *Pseudomonas* Resistant EST Library.

Directionally cloned cDNAs inserted into pBluescript

SK(-) at 5' end with EcoRI and 3' end with XhoI site."

## ORIGIN

Query Match 86.3%; Score 16.4; DB 1; Length 539;  
 Best Local Similarity 94.4%; Pred. No. 1e+03;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCGGGGACGATGACATT 18

|||||

Db 455 CCGGGGACGATGACTT 438

## RESULT 13

Bi627185 554 bp mRNA linear EST 07-SEP-2001  
 LOCUS RH68421.Sprime RH *Drosophila* melanogaster normalized Head pFlc-1  
 DEFINITION *Drosophila* melanogaster cDNA clone RH68421 5 similar to igl:  
 Fban018285 GO: (ligand binding or carrier (GO:0005488); calmodulin  
 binding (GO:0005516)) located on: 2R 51E5-51E7; : 08/24/2001, mRNA  
 sequence.

ACCESSION Bi627185

VERSION Bi627185.1 GI:15522710

KEYWORDS EST.

SOURCE *Drosophila* melanogaster (fruit fly)

ORGANISM *Drosophila* melanogaster

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; *Drosophila*.

1 (bases 1 to 554)

Stapleton, M., Brokstein, P., Hong, L., Tyler, D., Berman, B.,

Carlson, J., Champagne, C., Chavez, C., Dorsett, V., Farfan, D., Frise, E.,

George, R., Gonzalez, M., Guarin, H., Harris, N., Li, P., Liao, G.,

Misra, S., Mungall, C.J., Nunoo, J., Pacleb, J., Paragas, V., Park, S.,

Pouanenavong, S., Wan, K., Yu, C., Lewis, S.E., Celniker, S. and

Rubin, G.M.

TITLE BDGP/HMI RH *Drosophila* EST Project

JOURNAL Unpublished (2001)

COMMENT Contact: Stapleton, M.

BDGP

Lawrence Berkeley National Lab

One Cyclotron Rd, Berkeley, CA 94720, USA

Fax: 510 486 6798

Email: [http://www.fruitfly.org/EST\\_est@fruitfly.berkeley.edu](http://www.fruitfly.org/EST_est@fruitfly.berkeley.edu)

Plate: RH.684 row: B column: 9

High quality sequence stop: 462.

Location/Qualifiers

1..554

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 /clone\_lib="RH *Drosophila* melanogaster normalized Head  
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 /note="Organ: head; Vector: pFlc1; Site 1: XhoI; Site 2:  
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 the RIKEN. The library was normalized and excised using  
 Cre recombinase. Plasmid cDNA library."

## ORIGIN

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Db 456 CCGGGGACGATGACATT 473

## RESULT 14

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 ACCESSION AW963853  
 VERSION AW963853.1 GI:8153689  
 KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 562)

Hegde, P., Qi, R., Abernathy, K., Dharap, S., Gaspard, R., Gay, C.,

Holt, I.E., Saeed, A.I., Sharov, V., Lee, N.H., Yeatman, T.J. and

Quackenbush, J.

Assessment of gene expression patterns in a model of colon tumor

metastasis using a 19,200 element cDNA microarray

Unpublished (2000)

Contact: John Quackenbush

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 3528

Fax: 301 838 0208

Email: [johnq@tigr.org](mailto:johnq@tigr.org)

Plate: 194

Seq primer: Reverse.

Location/Qualifiers

1..562

/organism="Homo sapiens"

/mol\_type="mRNA"

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/clone\_lib="MAGE resequences, MAGH"

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ORIGIN

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 Best Local Similarity 94.4%; Pred. No. 1e+03;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCGGGGACGATGACATT 18

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Db 62 CCGGGGACGATGACATT 45

## RESULT 15

CO598991/c 594 bp mRNA linear EST 21-JUL-2004  
 LOCUS DG8-374n16 DG8-testis *Canis familiaris* cDNA 3', mRNA sequence.  
 DEFINITION  
 ACCESSION CO598991  
 VERSION CO598991.1 GI:50444555  
 KEYWORDS EST.

SOURCE *Canis familiaris* (dog)



ORGANISM Canis familiaris  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
REFERENCE 1 (bases 1 to 594)  
AUTHORS Schluter, T., Hermanns, J., Weindel, M., Schuette, D., Kranz, H.,  
Henrich, J. and Loebbert, R.  
TITLE Dog arrayTAG cDNA clone collection  
JOURNAL Unpublished (2004)  
COMMENT Contact: Thomas Schluter  
LION bioscience AG  
Waldhoferstrasse 98, D-69123 Heidelberg, Germany  
Tel: +49 6221 4038 150  
Fax: +49 6221 4038 290  
Email: Thomas.Schluter@lionbioscience.com.

FEATURES  
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Db 407 CCGGGGACGTTGACATTA 390

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Job time : 1746 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 12, 2005, 10:02:04 ; Search time 6689 Seconds  
(without alignments)  
11054.367 Million cell updates/sec

Title: US-09-979-558A-1  
Perfect score: 1526  
Sequence: 1 ttgatcatggctccagatt.....acctgcggctggatcaactc 1526

Scoring table: OligoNUC 5  
Gapop 60.0 , Gapext 60.0

Searched: 4708233 seqs, 24227607955 residues

Word size : 0

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : GenEmbl.\*

- 1: gb\_ba.\*
- 2: gb\_htg.\*
- 3: gb\_in.\*
- 4: gb\_om.\*
- 5: gb\_ov.\*
- 6: gb\_pat.\*
- 7: gb\_ph.\*
- 8: gb\_pl.\*
- 9: gb\_pr.\*
- 10: gb\_to.\*
- 11: gb\_sts.\*
- 12: gb\_by.\*
- 13: gb\_un.\*
- 14: gb\_vl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1526	100.0	1526	1	AB016057 Psychroba
2	1526	100.0	1526	6	E58427 DNA probe f
3	1124	73.7	1520	1	AB016059 Psychroba
4	1098	72.0	1473	1	AJ551093 Psychroba
5	1091	71.5	1473	1	AJ551098 Psychroba
6	1047	68.6	1473	1	AJ551101 Psychroba
7	1004	65.8	1403	1	AB094456 Psychroba
8	971	63.6	1531	1	AB016055 Psychroba
9	953	62.5	995	1	AF194191 Unculture
10	856	56.1	1530	1	AB016058 Psychroba
11	655	42.9	1684	1	AJ551107 Psychroba
12	646	42.3	1536	1	AB016054 Psychroba
13	566	37.1	1425	1	AF505739 Bacterium
14	566	37.1	1441	1	AF165598 Unculture
15	566	37.1	1445	1	AF468383 Arctic se
16	566	37.1	1449	1	AF165583 Psychroba
17	566	37.1	1459	1	AY167310 Psychroba
18	566	37.1	1463	1	AY167301 Psychroba
19	566	37.1	1476	1	AF505743 Bacterium

20	566	37.1	1483	1	AF468396	Arctic se
21	566	37.1	1485	1	AY167308	Psychroba
22	566	37.1	1493	1	AF505746	Gamma pro
23	566	37.1	1498	1	PGL313425	Psychroba
24	553	36.2	1462	1	AB094458	Psychroba
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28	515	33.7	1462	1	PGU85879	Psychroba
29	515	33.7	1539	1	AY573041	Psychroba
30	508	33.3	704	1	PSP244770	Psychroba
31	485	31.8	700	1	PSP244767	Psychroba
32	485	31.8	705	1	PSP244771	Psychroba
33	484	31.7	1454	1	AY167289	Psychroba
34	473	31.0	1478	1	AF517755	Psychroba
35	472	30.9	1475	1	AY443042	Psychroba
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40	435	28.5	1426	1	PSP272303	Psychroba
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42	416	27.3	1489	1	AY167286	Psychroba
43	413	27.1	1462	1	PGU85877	Psychroba
44	412	27.0	1525	1	AB016056	Psychroba
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ALIGNMENTS

AB016057 1526 bp DNA linear BCT 10-MAY-2000  
Psychrobacter pacificensis DNA for 16S rRNA, partial sequence,  
strain:NIBH P2K6(T) (=IFO 16279 (T)).

ACCESSION AB016057.1 GI:6691638

VERSION 16S ribosomal RNA.

KEYWORDS Psychrobacter pacificensis

SOURCE Psychrobacter pacificensis

ORGANISM Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Moraxellaceae; Psychrobacter.

REFERENCE 1 (sites)

AUTHORS Maruyama,A., Honda,D., Yamamoto,H., Kitamura,K. and Higashihara,T.

TITLE Phylogenetic analysis of psychrophilic bacteria isolated from the

Japan Trench, including a description of the deep-sea species

JOURNAL Psychrobacter pacificensis sp. nov

MEDLINE Int. J. Syst. Evol. Microbiol. 50 Pt 2, 835-846 (2000)

PUBMED 20222194

REFERENCE 2 (bases 1 to 1526)

AUTHORS Maruyama,A. and Kitamura,K.

TITLE Direct Submission

JOURNAL Submitted (07-JUL-1998) Akihiko Maruyama, National Institute of

Bioscience and Human-Technology, Department of Applied and

Environmental Microbiology; 1-1 Higashi, Tsukuba, Ibaraki 305-8566,

Japan (E-mail:maruyama@nibh.go.jp, Tel:+81-298-54-6062,

Fax:+81-298-54-8412)

FEATURES

source

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/mol\_type="genomic DNA"

/strain="NIBH P2K6(T) (=IFO 16279(T))"

/db\_xref="taxon:112002"

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/product="16S ribosomal RNA"

ORIGIN

Query Match 100.0%; Score 1526; DB 1; Length 1526;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
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DEFINITION DNA probe for detecting novel psychrophile.
ACCESSION E58427
VERSION E58427.1 GI:18622289
KEYWORDS JP 2000333680-A/1.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 1526)
AUTHORS Maruyama, A., Kitamura, K. and Kurane, R.
TITLE DNA probe for detecting novel psychrophile
JOURNAL Patent: JP 2000333680-A 1 05-DEC-2000;
COMMENT AGENCY OF IND SCIENCE & TECHNOL
OS Psychrobacter pacificus
PN JP 2000333680-A/1
PD 05-DEC-2000
PF 25-MAY-1999 JP 1999145342
PI AKIHIKO MARUYAMA, KEIKO KITAMURA, RYUICHIRO KURANE PC
C12N15/09, C12N1/20, C12Q1/68// (C12N15/09, C12R1:01), (C12N1/20, PC
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RESULT 3  
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DEFINITION  
 ACCESSION AB016059  
 VERSION AB016059.1 GI:6691640  
 KEYWORDS 16S ribosomal RNA.  
 SOURCE Psychrobacter pacificensis  
 ORGANISM Psychrobacter pacificensis  
 Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Moraxellaceae; Psychrobacter.

REFERENCE  
 1 (sites)  
 Maruyama, A., Honda, D., Yamamoto, H., Kitamura, K. and Higashihara, T. Phylogenetic analysis of psychrophilic bacteria isolated from the Japan Trench, including a description of the deep-sea species Psychrobacter pacificensis sp. nov. Int. J. Syst. Evol. Microbiol. 50 Pt 2, 835-846 (2000) 20222194  
 PUBMED 10758895

REFERENCE  
 2 (bases 1 to 1520)  
 Maruyama, A. and Kitamura, K. Direct Submission  
 Submitted (07-JUL-1998) Akihiko Maruyama, National Institute of Bioscience and Human-Technology, Department of Applied and Environmental Microbiology; 1-1 Higashi, Tsukuba, Ibaraki 305-8566, Japan (E-mail:maruyama@nibh.go.jp, Tel: +81-298-54-6062, Fax: +81-298-54-6412)

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VERSION AJ551093.1 GI:34525808
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SOURCE Psychrobacter sp. wp8
ORGANISM Psychrobacter sp. wp8
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Moraxellaceae; Psychrobacter.

REFERENCE
1 Wang, F., Wang, P., Chen, M. and Xiao, X.
Isolation of extremophiles with the detection and retrieval of
Shewanella strains in deep-sea sediments from the west Pacific
Extremophiles 8 (2), 165-168 (2004)
JOURNAL
PUBMED 15064982
REFERENCE
2 (bases 1 to 1473)
Xiao, X.
Direct Submission
Submitted (22-FEB-2003) Xiao X., Key Lab of Marine Biogenetic
Resources, Third Institute of Oceanography, SOA, Daxuelu 178,
Xiamen, 361005, CHINA
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Psychrobacter sp. wpl8
Psychrobacter sp. wpl8
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Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Moraxellaceae; Psychrobacter.
REFERENCE
1
Wang, F., Wang, P., Chen, M. and Xiao, X.

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TITLE
JOURNAL
PUBMED
REFERENCE
AUTHORS
Xiao, X.
Direct Submission
Submitted (22-FEB-2003) Xiao X., Key Lab of Marine Biogenetic
Resources, Third Institute of Oceanography, SOA, Daxueu 178,
Xiamen, 361005, CHINA
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Isolation of extremophiles with the detection and retrieval of
Shewanella strains in deep-sea sediments from the west Pacific
Extremophiles 8 (2), 165-168 (2004)
2 (bases 1 to 1473)
Xiao, X.
Direct Submission
Submitted (22-FEB-2003) Xiao X., Key Lab of Marine Biogenetic
Resources, Third Institute of Oceanography, SOA, Daxueu 178,
Xiamen, 361005, CHINA
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Submitted (23-OCT-2002) Fumio Inagaki, Japan Marine Science &				Qy	1275	AAAAGCCTATCGTAGTCCAGATTGGAGTCTCCAACTCGACTCCATGAAGTAGGAATCGCT	1334
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				Psychrobacter pacificensis			
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				Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;			
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				1 (sites)			
				Maruyama, A., Honda, D., Yamamoto, H., Kitamura, K. and Higashihara, T.			

TITLE Phylogenetic analysis of psychrophilic bacteria isolated from the Japan Trench, including a description of the deep-sea species *Psychrobacter pacificensis* sp. nov

JOURNAL Int. J. Syst. Evol. Microbiol. 50 Pt-2, 835-846 (2000)

MEDLINE 20222194

PUBMED 10758895

REFERENCE 2 (bases 1 to 1531)

AUTHORS Maruyama, A. and Kitamura, K.

TITLE Direct Submission

JOURNAL Submitted (07-JUL-1998) Akihiko Maruyama, National Institute of Bioscience and Human-Technology, Department of Applied and Environmental Microbiology; 1-1 Higashi, Tsukuba, Ibaraki 305-8566, Japan (E-mail:maruyama@nih.go.jp, Tel:+81-298-54-6062, Fax:+81-298-54-6412)

FEATURES

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509 AGCAGCCGCGGTATACAGAGGGTGCAAGCGTTAATCGGAATTACTGGGGGTAAAGCGAG 568

517 AGCAGCCGCGGTATACNAGAGGGTGCAAGCGTTAATCGGAATTACTGGGGGTAAAGCGAG 576

569 CGTAGTGGCTTGATAGTCAGATGTGAATCCCGGGCTTAACCTGGGAACCTGCATCTG 628

577 CGTAGTGGCTTGATAGTCAGATGTGAATCCCGGGCTTAACCTGGGAACCTGCATCTG 636

629 AACTGTAGCTAGAGTGTAGAGGAGTGAATTTTCAGGTGAGCGGTGAATATGC 688

637 AACTGTAGCTAGAGTGTAGAGGAGTGAATTTTCAGGTGAGCGGTGAATATGC 696

689 GTAGAGTCTGAAGGAATACCGATGGCGAAGGACGCTTCCTGGCATCATACTGACACTGA 748

697 GTAGAGTCTGAAGGAATACCGATGGCGAAGGACGCTTCCTGGCATCATACTGACACTGA 756

749 GGCTCGAAGGCTGGGTAGCAACAGATTAGATACCTGTGTAGTCCACGCGGTAAACGA 808

757 GGCTCGAAGGCTGGGTAGCAACAGATTAGATACCTGTGTAGTCCACGCGGTAAACGA 816

809 TGTCTACTAGTCGTTGGTCCCTTGTAGGACTTGTAGCGAGCTTAAGCGAATAGTAGAC 868

817 TGTCTACTAGTCGTTGGTCCCTTGTAGGACTTGTAGCGAGCTTAAGCGAATAGTAGAC 876

869 CGCTGGGGAGTACGGCCGCAAGGTTAAACTCAATGAATTTGACGGGGGCCGCAACAG 928

877 CGCTGGGAGTAGCGCGCAAGGTTAAAACTCAATGAATTGACGGGGCCGCCACAAG 936

929 CGGTGAGCATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCTGCTTGGATAC 988

937 CGGTGAGCATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCTGCTTGGATAC 996

989 ACAGAACTTTGTAGATACGAGAGTGCCTTCGGGAATTGTGATACAGGTGCTGCATGGC 1048

997 ACAGAACTTTGTAGATACGAGAGTGCCTTCGGGAATTGTGATACAGGTGCTGCATGGC 1056

1049 TGTGTCAGCTCGTGTGTCGAGATGTTGGTTAAGTCCCGCAACGCGAACCCTTGTGTC 1108

1057 TGTGTCAGCTCGTGTGTCGAGATGTTGGTTAAGTCCCGCAACGAGCGC-ANCCTTGTC 1115

1109 CTTAGTTACAGCACTTCGGTGGGAACCTTAAGGATCTTAAGGATGACAGTGCATGGAGGA 1168

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1176 AGCGGGGACGACGTCGAAGTCATCGCCCTTACGACAGGCTACACACGTCGTACAA 1235

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1296 GTCCAGATTGGAGTCTGCAACTCGACTCCATGAAGTAGGAATCGTAGTAATCGCGATC 1355

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1356 AGAATGCCGGGTGAATACATGTTCCCGGCCCTGTACACACCGCCCGTACACCATGGGAG 1415

1409 TTGATTGCACAGAAAGTGTGATCGCTTAACCTTAGTGGGCGATCACACCGTGTGTCGA 1468

1416 TTGATTGCACAGAAAGTGTGATCGCTTAACCTTAGTGGGCGATCACACCGTGTGTCGA 1475

1469 TGACTGGGTGAAGTGTGAACAGGTAGCGTAGGG 1504

1476 TGACTGGGTGAAGTGTGAACAGGTAGCGTAGGG 1511

RESULT 9

AF194191 LOCUS Uncultured Psychrobacter a2 16S ribosomal RNA gene, partial sequence.

DEFINITION

AF194191 ACCESSION

AF194191.1 GI:8101556 VERSION

uncultured Psychrobacter a2 KEYWORDS

uncultured Psychrobacter a2 ORGANISM

Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Moraxellaceae; Psychrobacter; environmental samples.

REFERENCE 1 (bases 1 to 995)

AUTHORS Todorov, J.R., Chistoserdov, A.Y. and Aller, J.Y.

TITLE Molecular analysis of microbial communities in mobile deltaic muds of Southeastern Papua New Guinea

JOURNAL FEMS Microbiol. Ecol. 33 (2), 147-155 (2000)

PUBMED 10967214

REFERENCE 2 (bases 1 to 995)

AUTHORS Todorov, J.R., Aller, J.Y. and Chistoserdov, A.Y.

TITLE Direct Submission

JOURNAL Submitted (13-OCT-1999) Marine Sciences Research Center, State University of New York at Stony Brook, Stony Brook, NY 11794-5000, USA

FEATURES

source Location/Qualifiers

1. .995

/organism="uncultured psychrobacter a2"

/mol\_type="genomic DNA"

/db\_xref="taxon:126515"

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/clone="a2"
/environmental_sample
<1..>995
/product="16S ribosomal RNA"

ORIGIN
Query/Match 62.5%; Score 953; DB 1; Length 995;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 953; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 513 GCCCGGTAAATACAGAGGTGCAAGCGTTAATCGGAATTACTGGCGGTAAGCGAGCGTA 572
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QY 573 GGTGGCTTGATAGTACAGATGCAATCCCGGGCTTAACCTGGGAATCGATCTCAAAAC 632
DB 70 GGTGGCTTGATAGTACAGATGCAATCCCGGGCTTAACCTGGGAATCGATCTCAAAAC 129
QY 633 TGTAGGCTAGATAGTACAGAGGAAAGTAGAATTTTCAGGTGTAGCGGTGAATCGGTAG 692
DB 130 TGTAGGCTAGATAGTACAGAGGAAAGTAGAATTTTCAGGTGTAGCGGTGAATCGGTAG 189
QY 693 AGATCTGAGGAATACCGATGCGAGGAGCGCTTCTGCGATCATACTACACTGAGGCT 752
DB 190 AGATCTGAGGAATACCGATGCGAGGAGCGCTTCTGCGATCATACTACACTGAGGCT 249
QY 753 CGAAAGCGTGGGTAGCAACACAGATTAGATACCTGGTAGTCCACGCCGTAAACGATGTC 812
DB 250 CGAAAGCGTGGGTAGCAACACAGATTAGATACCTGGTAGTCCACGCCGTAAACGATGTC 309
QY 813 TACTAGTCGTGGGTCCCTTGGAGTCTTAGTGACGAGCTAAACGCAATAGTACACGCC 872
DB 310 TACTAGTCGTGGGTCCCTTGGAGTCTTAGTGACGAGCTAAACGCAATAGTACACGCC 369
QY 873 TGGGAGTACGCCCGCAAGTTTAAACTCAATGATTAATGACGGGGCGCGCACAGCGGT 932
DB 370 TGGGAGTACGCCCGCAAGTTTAAACTCAATGATTAATGACGGGGCGCGCACAGCGGT 429
QY 933 GGAGCATGTGTTTAAATCGATGCAACGCGAAGAACCTTACCTGGTCTTGACATACACAG 992
DB 430 GGAGCATGTGTTTAAATCGATGCAACGCGAAGAACCTTACCTGGTCTTGACATACACAG 489
QY 993 AATCTTGTAGATACAGAGTGCCTTCGGGAATTTGTGATACAGTGTGATGCTGTC 1052
DB 490 AATCTTGTAGATACAGAGTGCCTTCGGGAATTTGTGATACAGTGTGATGCTGTC 549
QY 1053 GTCAGCTGTCGTCGATGTTGGTTAAGTCCCGCAACGAGCGCAACCTTGTGCTTA 1112
DB 550 GTCAGCTGTCGTCGATGTTGGTTAAGTCCCGCAACGAGCGCAACCTTGTGCTTA 609
QY 1113 GTTACAGCACCTTCGGGTGGGAATCTTAAGGATCTGCGAGTACCAAACTGGAGGAAGC 1172
DB 610 GTTACAGCACCTTCGGGTGGGAATCTTAAGGATCTGCGAGTACCAAACTGGAGGAAGC 669
QY 1173 GGGGACGACGTCAAGTCAATGTCGCTTACGACGAGGCTTACACAGTGTCTACAATGGT 1232
DB 670 GGGGACGACGTCAAGTCAATGTCGCTTACGACGAGGCTTACACAGTGTCTACAATGGT 729
QY 1233 AGGTACAGAGGCGACGTACAGCGATGTGATGCGAATCTCAAAAGCGCTATCGTAGTCC 1292
DB 730 AGGTACAGAGGCGACGTACAGCGATGTGATGCGAATCTCAAAAGCGCTATCGTAGTCC 789
QY 1293 AGATTGGAGTCTGCAACTCGACTCCATGAAGTGAAGTACGCTAGTAAATCGCGGATCAGAA 1352
DB 790 AGATTGGAGTCTGCAACTCGACTCCATGAAGTGAAGTACGCTAGTAAATCGCGGATCAGAA 849
QY 1353 TGC CGCGGTGAATACGTTTCCGGGCTTGTACACACCGCCCGTACACCATGGGAGTTGA 1412
DB 850 TGC CGCGGTGAATACGTTTCCGGGCTTGTACACACCGCCCGTACACCATGGGAGTTGA 909
QY 1413 TTGCAACGAGAGTGTGATGCTTAACTTAGTGAGGGCGGATCACACGTTGTGT 1465
DB 910 TTGCAACGAGAGTGTGATGCTTAACTTAGTGAGGGCGGATCACACGTTGTGT 962

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RESULT 10

AB016058

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

rRNA

ORIGIN

Query Match

Best Local Similarity

Matches 1096; Conservative

0; Mismatches

0; Indels

2; Gaps

QY

DB

QY

DB

QY

DB

QY

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QY

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QY

DB

AB016058

Psychrobacter pacificensis DNA for 16S rRNA, partial sequence,

strain:NIBH P2K17.

AB016058

16S ribosomal RNA.

Psychrobacter pacificensis

Psychrobacter pacificensis

Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;

Moraxellaceae; Psychrobacter.

1 (sites)

Maruyama, A., Honda, D., Yamamoto, H., Kitamura, K. and Higashihara, T.

Phylogenetic analysis of psychrophilic bacteria isolated from the

Japan Trench, including a description of the deep-sea species

Psychrobacter pacificensis sp. nov

Int. J. Syst. Evol. Microbiol. 50 Pt 2, 835-846 (2000)

20222194

10758895

2 (bases 1 to 1530)

Maruyama, A. and Kitamura, K.

Direct Submission

Submitted (07-JUL-1998) Akihiko Maruyama, National Institute of

Bioscience and Human-Technology, Department of Applied and

Environmental Microbiology; 1-1 Higashi, Tsukuba, Ibaraki 305-8566,

Japan (E-mail:maruyama@nibh.go.jp, Tel: +81-298-54-6062,

Fax: +81-298-54-6412)

Location/Qualifiers

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/organism="Psychrobacter pacificensis"

/mol\_type="genomic DNA"

/strain="NIBH P2K17"

/db\_xref="taxon:112002"

<1..>1530

/product="16S ribosomal RNA"

Query Match 56.1%; Score 856; DB 1; Length 1530;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 1096; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

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DB

QY

DB

QY

DB

QY

DB

QY

DB

QY

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QY

DB

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DB

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DB

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DB

QY

DB

QY

DB

QY

DB

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Qy 848 CAGCTAACGCAATAGTAGACCGCTCGGGAGTAGCGCGCAAGTTTAAACTCAAATGA 907
Db 849 CAGCTAACGCAATAGTAGACCGCTCGGGAGTAGCGCGCAAGTTTAAACTCAAATGA 908
Qy 908 ATTACAGGGGCGCGCACAGCGGTGGAGCATGTTGTTTAATTCGATGCAACGCGAAGAA 967
Db 909 ATTACAGGGGCGCGCACAGCGGTGGAGCATGTTGTTTAATTCGATGCAACGCGAAGAA 968
Qy 968 CTTTACCTGTTCTTGACATACACAGAATCTTGTAGAGATACGAGAGTGCCTTCGGGAATT 1027
Db 969 CTTTACCTGTTCTTGACATACACAGAATCTTGTAGAGATACGAGAGTGCCTTCGGGAATT 1027
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Db 1028 GTGATACAGGTGTCGATGCTGTCGTCAGCTCGTGTGAGATGTTGGGTTAAAGTCCC 1087
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Qy 1148 TGCCAGTGACAACTGGAGGAAGCGGAGCGAGTCAAGTCATCATGGCCCTTACGACC 1207
Db 1148 TGCCAGTGACAACTGGAGGAAGCGGAGCGAGTCAAGTCATCATGGCCCTTACGACC 1207
Qy 1208 AGGCTACACACGTCGTACAAATGGTAGGTACAGAGGCGAGCTACACAGCGATGTGATGCG 1267
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Db 1268 AATCTCAAAAGCCTATCTAGTCCAGATTGGAGTCTGCAACTCGACTCCATGGAAGTAGG 1327
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Db 1328 AATCGCTAGTAATCCGCGATCAGAAATCCGCGGTGAATACGTTCCCGGGCCTTGACACA 1387
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Qy 1448 CGATCACCACGGTGTGGT 1465
Db 1448 CGATCACCACGGTGTGGT 1465
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RESULT 11
PSP51107 PSP51107 1684 bp DNA linear BCT 17-MAY-2004
LOCUS Psychrobacter sp. wp30 partial 16S rRNA gene, isolate wp30.
DEFINITION
ACCESSION AJ551107
VERSION AJ551107.1 GI:34525821
KEYWORDS 16S ribosomal RNA; 16S rRNA gene.
SOURCE Psychrobacter sp. wp30
ORGANISM Psychrobacter sp. wp30
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Moraxellaceae; Psychrobacter.
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REFERENCE 1
AUTHORS Wang, F., Wang, P., Chen, M. and Xiao, X.
TITLE Isolation of extremophiles with the detection and retrieval of
JOURNAL Shewanella strains in deep-sea sediments from the west Pacific
PUBMED Extremophiles 8 (2), 165-168 (2004)
REFERENCE 2 (bases 1 to 1684)
AUTHORS Xiao, X.
TITLE Direct Submission
JOURNAL Submitted (22-FEB-2003) Xiao X., Key Lab of Marine Biogenetic
Resources, Third Institute of Oceanography, SOA, Daxuelu 178,
Xiamen, 361005, CHINA
FEATURES Location/Qualifiers
source 1..1684
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/organism="Psychrobacter sp. wp30"
/mol_type="genomic DNA"
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/isolation_source="deep sea sediment"
/db_xref="taxon:225865"
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/gene="16S rRNA"
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/gene="16S rRNA"
/product="16S ribosomal RNA"
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Query Match 42.9%; Score 655; DB 1; Length 1684;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 655; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 368 GGGAAACCCCTGATCCAGCATGCGCGGTGTGTAAGAAGGCGCTTTGGTTGTAAGCACTT 427
Db 383 GGGAAACCCCTGATCCAGCATGCGCGGTGTGTAAGAAGGCGCTTTGGTTGTAAGCACTT 442
Qy 428 TAAGCAGTGAAGAAGACTCTTCGGTTAATACCCGGGACGATGACATTAGCTGCAGAATA 487
Db 443 TAAGCAGTGAAGAAGACTCTTCGGTTAATACCCGGGACGATGACATTAGCTGCAGAATA 502
Qy 488 AGCACGGCTAACTCTGTGCCAGCAGCGCGGTAAATACAGAGGGTGCAGCGTTAATCGG 547
Db 503 AGCACGGCTAACTCTGTGCCAGCAGCGCGGTAAATACAGAGGGTGCAGCGTTAATCGG 562
Qy 548 AATTACTGGCGTAAAGCGAGCGTAGTGGCTTGATAAGTCAGATGTGAATCCCCGGGC 607
Db 563 AATTACTGGCGTAAAGCGAGCGTAGTGGCTTGATAAGTCAGATGTGAATCCCCGGGC 622
Qy 608 TTAACTGGGAACTGCATCTGAAACTGTGTTAGGCTAGAGTAGGTGAGAGGAAGTAGAATT 667
Db 623 TTAACTGGGAACTGCATCTGAAACTGTGTTAGGCTAGAGTAGGTGAGAGGAAGTAGAATT 682
Qy 668 TCAGGTCTAGCGGTGAATCCGCTAGAGATCTGAAGGAATACCGATGCGAGGCGAGCTTC 727
Db 683 TCAGGTCTAGCGGTGAATCCGCTAGAGATCTGAAGGAATACCGATGCGAGGCGAGCTTC 742
Qy 728 CTGGCATCATCTACACACCTGAGGCTCGAAAGCGTGGGTAGCAACAGGATTAGATACCCT 787
Db 743 CTGGCATCATCTACACACCTGAGGCTCGAAAGCGTGGGTAGCAACAGGATTAGATACCCT 802
Qy 788 GGTAGTCCACGCGTAAACGATGTCTACTAGTGTGGTCCCTTGAAGGACTTAGTGACG 847
Db 803 GGTAGTCCACGCGTAAACGATGTCTACTAGTGTGGTCCCTTGAAGGACTTAGTGACG 862
Qy 848 CAGCTAACGCAATAGTAGACCGCTGGGAGTAGCGCGCAAGGTTTAAAACTCAAATGA 907
Db 863 CAGCTAACGCAATAGTAGACCGCTGGGAGTAGCGCGCAAGGTTTAAAACTCAAATGA 922
Qy 908 ATTACAGGGGCGCGCACAGCGGTGGAGCATGTTGTTTAATTCGATGCAACGCGAAGAA 967
Db 923 ATTACAGGGGCGCGCACAGCGGTGGAGCATGTTGTTTAATTCGATGCAACGCGAAGAA 982
Qy 968 CTTTACCTGTTCTTGACATACACAGAATCTTGTAGAGATACGAGAGTGCCTTCGG 1022
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## RESULT 12

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DEFINITION strain:NIBH P202.
ACCESSION AB016054
VERSION AB016054.1 GI:6691635
KEYWORDS 16S ribosomal RNA.
SOURCE Psychrobacter pacificensis
ORGANISM Psychrobacter pacificensis
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
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Db	974	CCGGTCTTGACATACACAGAACTCTGTAGAGATACAGAGATGCGCTTCGGGAATTGTGATA	103			
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Db	1034	CAGGTGCTGCATGGCTGTTCGTCACTCGTGTCTGTGAGATGTTGGTTAAAGTCCGCAACG	1093			
Qy	1094	AGCGCAACCCCTTGCTCTTAGTTACCAGC	1121			
Db	1094	AGCGCAACCCCTTGCTCTTAGTTACCAGC	1121			
RESULT 13						
AF505739						
LOCUS	AF505739	1425 bp	DNA linear BCT 31-JAN-2003			
DEFINITION	Bacterium UMB10E 16S ribosomal RNA gene, partial sequence.					
ACCESSION	AF505739					
VERSION	AF505739.1 GI:28173016					
KEYWORDS	bacterium UMB10E					
SOURCE	bacterium UMB10E					
ORGANISM	Bacteria.					
REFERENCE	1 (bases 1 to 1425)					
AUTHORS	Tang,R.J. and Cooney,J.J.					
TITLE	Tributyltin-resistent, biofilm-forming bacteria isolated from Boston Harbor, MA					
JOURNAL	Unpublished					
REFERENCE	2 (bases 1 to 1425)					
AUTHORS	Tang,R.J. and Cooney,J.J.					
TITLE	Direct Submission					
JOURNAL	Submitted (23-APR-2002) Environmental, Coastal and Ocean Sciences, University of Massachusetts Boston, 100 Morrissey Blvd., Boston, MA 02125-3393, USA					
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/notes="tributyltin-resistant strain"						
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Best Local Similarity 99.8%; Pred. No. 0;						
Matches 616; Conservative 0; Mismatches 1; Indels 0; Gaps 0;						
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Qy	431	GCAGTGAAGAAGACTCTTCGGTTAATACCCGGGAGCGATGACATTAGTCGAGATAAGC	490			
Db	385	GCAGTGAAGAAGACTCTTCGGTTAATACCCGGGAGCGATGACATTAGTCGAGATAAGC	444			
Qy	491	ACCGGTAACTCTGTGCCAGACGCCGGGTAAATACAGAGGGTCAACCGTTATCGGAAT	550			
Db	445	ACCGGTAACTCTGTGCCAGACGCCGGGTAAATACAGAGGGTCAACCGTTATCGGAAT	504			
Qy	551	TACTGGCGGTAAAGCAGCGGTAGTGGCTTGTATAAGTCAGATGTGAAATCCCCGGGCTTA	610			
Db	505	TACTGGCGGTAAAGCAGCGGTAGTGGCTTGTATAAGTCAGATGTGAAATCCCCGGGCTTA	564			
Qy	611	ACCTGGGAACTGCATCTGAAACTGTTAGGCTAGAGTAGGTGAGAGGGAAGTAGAATTTCA	670			
Db	565	ACCTGGGAACTGCATCTGAAACTGTTAGGCTAGAGTAGGTGAGAGGGAAGTAGAATTTCA	624			
Qy	671	GGTGTAACGGTGAATGCGTAGAGATCTGAAGAAATACCGATGGCAGGACGCTTCCTG	730			
Db	625	GGTGTAACGGTGAATGCGTAGAGATCTGAAGAAATACCGATGGCAGGACGCTTCCTG	684			

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Qy 731 GCATCATACTGACACTGAGGCTCGAAAGCGTGGGTAGCAAAAGGATTAGATACCCCTGGT 790
Db 685 GCATCATACTGACACTGAGGCTCGAAAGCGTGGGTAGCAAAAGGATTAGATACCCCTGGT 744
Qy 791 AGTCACGCCGTAACCATGCTACTAGTCTGGGTCCCTTGGAGACTTAGTGACGCAG 850
Db 745 AGTCACGCCGTAACCATGCTACTAGTCTGGGTCCCTTGGAGACTTAGTGACGCAG 804
Qy 851 CTAAACGCAATAAGTAGACCTGGGAGTAGTACCGCCCAAGGTTAAAACCTCAAATGAATT 910
Db 805 CTAAACGCAATAAGTAGACCTGGGAGTAGTACCGCCCAAGGTTAAAACCTCAAATGAATT 864
Qy 911 GACGGGGCCCGCACACAGCGGTGAGCATGTGGTTTAAATTCGATGCAACGCGAAGACCT 970
Db 865 GACGGGGCCCGCACACAGCGGTGAGCATGTGGTTTAAATTCGATGCAACGCGAAGACCT 924
Qy 971 TACCTGGTCTTGACATA 987
Db 925 TACCTGGTCTTGACATA 941

RESULT 14
LOCUS AV165598 1441 bp DNA linear BCT 06-NOV-2003
DEFINITION Uncultured Arctic sea ice bacterium clone ARXVI/2-136 16S
            ribosomal RNA gene, partial sequence.
ACCESSION AV165598
VERSION AV165598.1 GI:28624892
KEYWORDS uncultured Arctic sea ice bacterium
SOURCE uncultured Arctic sea ice bacterium
ORGANISM Bacteria; environmental samples.
REFERENCE 1 (bases 1 to 1441)
AUTHORS Brinkmeyer,R., Knittel,K., Jurgens,J., Weyland,H., Amann,R. and
            Helme,E.
TITLE Diversity and Structure of Bacterial Communities in Arctic versus
            Antarctic Pack Ice
JOURNAL Appl. Environ. Microbiol. 69 (11), 6610-6619 (2003)
PUBMED 14602620
REFERENCE 2 (bases 1 to 1441)
AUTHORS Brinkmeyer,R., Knittel,K., Juergens,J., Weyland,H., Amann,R. and
            Helme,E.
TITLE Direct Submission
JOURNAL Submitted (17-OCT-2002) Alfred Wegener Institute for Polar and
            Marine Research, Am Handelshafen 12, Bremerhaven D-27570, Germany
FEATURES
            Location/Qualifiers
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rRNA
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Query Match 37.1%; Score 566; DB 1; Length 1441;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 616; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 371 AACCTGATCAGGCATGCCGCGTGTGTAAGAGGCGCTTTGGTTGTAAGCACTTTAA 430
Db 348 AACCTGATCAGGCATGCCGCGTGTGTAAGAGGCGCTTTGGTTGTAAGCACTTTAA 407
Qy 431 GCAGTGAAGAGACTCTTCGGTTAATACCCGGGACCATGACATTAGCTGCAGATAAGC 490
Db 408 GCAGTGAAGAGACTCTTCGGTTAATACCCGGGACCATGACATTAGCTGCAGATAAGC 467
Qy 491 ACCGGCTAACTCTGTGCGCAGCAGCGCGGTAAATACAGAGGTTGCAACGCTTAATCGGAAT 550

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Db 468 ACCGGCTAACTCTGTGCCACAGCCCGCGGTAAATACAGAGGTCGAAGCGTTAATCGGAAT 527
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Db 528 TACTGGCGTAAAGCGAGCGTAGTGGCTTTGATATAAGTCAGATGTGAAATCCCGGGCTTA 587
Qy 611 ACCTGGGAACCTGCATCTGAAACCTGTTAGGCTAGAGTAGGTGAGAGGGAAGTAGAATTTC 670
Db 588 ACCTGGGAACCTGCATCTGAAACCTGTTAGGCTAGAGTAGGTGAGAGGGAAGTAGAATTTC 647
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Db 648 GGTGTAGCGGTGAAATCGGTAGAGATCTGAAAGGAATACCGATGCGCAAGCAGCTTCCTG 707
Qy 731 GATCATACTGACACTGAGGCTCGAAAGCGTGGGTAGCAAAAGGATTAGATACCCCTGGT 790
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Qy 791 AGTCCACGCGGTAAACGATGCTACTAGTGTGGGTCCCTTGAGGACTTAGTGACGCAG 850
Db 768 AGTCCACGCGGTAAACGATGCTACTAGTGTGGGTCCCTTGAGGACTTAGTGACGCAG 827
Qy 851 CTAAACGCAATAAGTAGACCTGGGAGTAGTACCGCCCAAGGTTAAAACCTCAAATGAATT 910
Db 828 CTAAACGCAATAAGTAGACCTGGGAGTAGTACCGCCCAAGGTTAAAACCTCAAATGAATT 887
Qy 911 GACGGGGCCCGCACACAGCGGTGAGCATGTGGTTTAAATTCGATGCAACGCGAAGACCT 970
Db 888 GACGGGGCCCGCACACAGCGGTGAGCATGTGGTTTAAATTCGATGCAACGCGAAGACCT 947
Qy 971 TACCTGGTCTTGACATA 987
Db 948 TACCTGGTCTTGACATA 964

RESULT 15
LOCUS AF468383 1445 bp DNA linear BCT 06-NOV-2003
DEFINITION Arctic sea ice bacterium ARK10009 16S ribosomal RNA gene, partial
            sequence.
ACCESSION AF468383
VERSION AF468383.1 GI:28269031
KEYWORDS Arctic sea ice bacterium ARK10009
SOURCE Arctic sea ice bacterium ARK10009
ORGANISM Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
            Moraxellaceae; Psychrobacter.
REFERENCE 1 (bases 1 to 1445)
AUTHORS Brinkmeyer,R., Knittel,K., Jurgens,J., Weyland,H., Amann,R. and
            Helme,E.
TITLE Diversity and Structure of Bacterial Communities in Arctic versus
            Antarctic Pack Ice
JOURNAL Appl. Environ. Microbiol. 69 (11), 6610-6619 (2003)
PUBMED 14602620
REFERENCE 2 (bases 1 to 1445)
AUTHORS Brinkmeyer,R. and Helme,E.
TITLE Direct Submission
JOURNAL Submitted (15-JAN-2002) Pelagic Oceanography,
            Alfred-Wegener-Institut fuer Polar und Meeresforschung, Am
            Handelshafen 12, Bremerhaven D-27570, Germany
FEATURES
            Location/Qualifiers
                1..1445
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                /mol_type="genomic DNA"
                /isolate="ARK10009"
                /isolation_source="Arctic sea ice"
                /db_xref="taxon:196809"
                <1..>1445
                /product="16S ribosomal RNA"

rRNA
ORIGIN
Query Match 37.1%; Score 566; DB 1; Length 1445;
Best Local Similarity 99.8%; Pred. No. 0;

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Matches 616; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
Qy	371 AACCTGATCCAGCCATCCGCGTGTGTGAAGAAGCCCTTTTGGTTGTAAAGCACTTTAA 430
Db	
Qy	329 AACCTGATCCAGCCATCCGCGTGTGTGAAGAAGCCCTTTTGGTTGTAAAGCACTTTAA 388
Db	
Qy	431 GCAGTGAAGAAGACTCTTCGGTTAATACCCGGGACGATGACATTTAGCTGCAGATAAGC 490
Db	
Qy	389 GCAGTGAAGAAGACTCTTCGGTTAATACCCGGGACGATGACATTTAGCTGCAGATAAGC 448
Db	
Qy	491 ACCGGCTAACTCTGTGCCAGAGCCGCGTGAATACAGAGGGTGCAGCGTTAATCGGAAT 550
Db	
Qy	449 ACCGGCTAACTCTGTGCCAGAGCCGCGTGAATACAGAGGGTGCAGCGTTAATCGGAAT 508
Db	
Qy	551 TACTGGGCGTAAAGCGAGCTAGGTGGCTTGATAGTCAGATGTGAAATCCCGGGCTTA 610
Db	
Qy	509 TACTGGGCGTAAAGCGAGCTAGGTGGCTTGATAGTCAGATGTGAAATCCCGGGCTTA 568
Db	
Qy	611 ACCTGGGAATGCTGATCTGAAACTGTTAGGCTAGTAGGTGAGAGGGGAAGTAGAATTCA 670
Db	
Qy	569 ACCTGGGAATGCTGATCTGAAACTGTTAGGCTAGTAGGTGAGAGGGGAAGTAGAATTCA 628
Db	
Qy	671 GGTGTAGCGGTCAATGCTGAGATCTGAAGGATACCGATGGCGRAGGCAGCTTCCTG 730
Db	
Qy	629 GGTGTAGCGGTCAATGCTGAGATCTGAAGGATACCGATGGCGRAGGCAGCTTCCTG 688
Db	
Qy	731 GCATCATACTGACACTGAGGCTCGAAAGCGTGGGTAGCAACAGGATTAGATACCCCTGGT 790
Db	
Qy	689 GCATCATACTGACACTGAGGCTCGAAAGCGTGGGTAGCAACAGGATTAGATACCCCTGGT 748
Db	
Qy	791 AGTCCACCCCGTAAACGATGTCTACTAGTCGTGGGTCCCTTGAGGACTTTAGTGACGCAG 850
Db	
Qy	749 AGTCCACCCCGTAAACGATGTCTACTAGTCGTGGGTCCCTTGAGGACTTTAGTGACGCAG 808
Db	
Qy	851 CTAACGCAATAAGTAGACCGCTCGGGAGTAGCGCCGCAAGTTTAAACTCAATGAATT 910
Db	
Qy	809 CTAACGCAATAAGTAGACCGCTCGGGAGTAGCGCCGCAAGTTTAAACTCAATGAATT 868
Db	
Qy	911 GACGGGGCCCGCACAAAGCGGTGGAGCATGTGGTTTAAATTCGATGCAACGGAAGAACCT 970
Db	
Qy	869 GACGGGGCCCGCACAAAGCGGTGGAGCATGTGGTTTAAATTCGATGCAACGGAAGAACCT 928
Db	
Qy	971 TACCTGGTCTTGACATA 987
Db	
Qy	929 TACCTGGTCTTGACATA 945
Db	

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Job time : 6693 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: April 12, 2005, 10:00:33 ; Search time 870 Seconds  
(without alignments)  
10383.362 Million cell updates/sec

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Perfect score: 1526  
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Scoring table: OLIGO\_NUC3  
Gapop 60.0 , Gapext 60.0

Searched: 4390206 seqs, 2959870667 residues

Word size : 0

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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- 2: geneseqn1990s:\*
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- 4: geneseqn2001as:\*
- 5: geneseqn2001bs:\*
- 6: geneseqn2002as:\*
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- 8: geneseqn2003as:\*
- 9: geneseqn2003bs:\*
- 10: geneseqn2003cs:\*
- 11: geneseqn2003ds:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1526	100.0	1526	4 AAC87531	AAC87531 Psychroba
2	136	8.9	1485	2 AAQ13256	AAQ13256 16S rRNA
3	136	8.9	269223	4 AAF28554	AAF28554 Genomic f
4	121	7.9	549	3 AAC95222	AAC95222 Cat flea
5	121	7.9	1487	5 AAS11034	AAS11034 Shigella
6	121	7.9	1489	6 ABS71622	ABS71622 Klebsiell
7	121	7.9	1506	6 ABS71613	ABS71613 Escherich
8	121	7.9	1533	13 ADQ81656	ADQ81656 Enterobac
9	121	7.9	1534	10 ADB61683	ADB61683 16S rRNA
10	121	7.9	1540	1 AAN91514	AAN91514 Escherich
11	121	7.9	1542	2 AAT29140	AAT29140 rRNA gene
12	121	7.9	1542	4 AAC62270	AAC62270 Escherich
13	121	7.9	1542	5 AAF23015	AAF23015 E. coli 1
14	121	7.9	1542	5 AAH75410	AAH75410 E. coli 1
15	121	7.9	1542	6 ABN85800	ABN85800 Escherich
16	121	7.9	1542	9 ADB16299	ADB16299 Cleavage
17	121	7.9	1542	9 AAD57988	AAD57988 Escherich
18	121	7.9	1542	10 ADC02547	ADC02547 E. coli r
19	121	7.9	1542	12 ADQ16352	ADQ16352 Nucleotid
20	121	7.9	1549	3 AAA65897	AAA65897 E. coli p

21	121	7.9	1549	3 AAA66050	AAA66050 E. coli p
22	121	7.9	1549	3 AAA66055	AAA66055 E. coli p
c 23	121	7.9	5090	2 AAX24988	AAX24988 E. coli M
24	121	7.9	5097	2 AAX24983	AAX24983 E. coli M
25	121	7.9	5098	2 AAX24984	AAX24984 E. coli M
26	121	7.9	5105	2 AAX24989	AAX24989 E. coli M
c 27	121	7.9	5341	2 AAX24986	AAX24986 E. coli M
c 28	121	7.9	7508	9 AAL62713	AAL62713 Escherich
c 29	121	7.9	10903	12 ADK51929	ADK51929 Novel rRN
c 30	121	7.9	11918	12 ADK51930	ADK51930 Novel rRN
31	121	7.9	13278	12 ADK51931	ADK51931 Novel rRN
32	116	7.6	1462	4 AAF85587	AAF85587 Pseudoalt
33	116	7.6	1474	6 AAF17194	AAF17194 Pseudoalt
34	116	7.6	1492	13 ADS52325	ADS52325 Pseudoalt
35	116	7.6	1494	8 ABX16332	ABX16332 Aliphatic
36	116	7.6	1528	2 AAX83570	AAX83570 16S rDNA
37	116	7.6	1529	2 AAX83564	AAX83564 16S rDNA
38	116	7.6	1529	2 AAX83566	AAX83566 16S rDNA
39	116	7.6	1529	2 AAX83565	AAX83565 16S rDNA
40	116	7.6	1529	2 AAX83567	AAX83567 16S rDNA
41	116	7.6	1535	2 AAX83568	AAX83568 16S rDNA
42	116	7.6	1535	2 AAX83569	AAX83569 16S rDNA
43	115	7.5	888	2 AAQ46120	AAQ46120 E. coli 1
44	115	7.5	1542	2 AAQ46119	AAQ46119 E. coli 1
45	114	7.5	1541	5 AAS11022	AAS11022 Salmonell

#### ALIGNMENTS

##### RESULT 1

AAC87531  
ID AAC87531 standard; DNA; 1526 BP.  
AC AAC87531;  
XX  
DT 13-MAR-2001 (first entry)  
XX Psychrobacter pacificensis NIBH P2K6 16S rDNA, SEQ ID NO:1.  
DE  
XX 16S rDNA; species-specific detection; identification;  
KW psychrophilic bacterium; oceanic circulation; Psychrobacter;  
KW strain NIBH P2K6; ds.  
XX  
OS Psychrobacter pacificensis.  
XX  
PN WO200071705-A1.  
XX  
PD 30-NOV-2000.  
XX  
PF 25-MAY-2000; 2000WO-JP003372.  
XX  
PR 25-MAY-1999; 99JP-00145342.  
XX 30-MAR-2000; 2000WO-JP002045.  
XX (AGEN ) AGENCY OF IND SCI & TECHNOLOGY.  
XX Maruyama A, Kitamura K, Kurane R;  
XX WPI; 2001-025158/03.  
XX  
XX DNA probe originating from psychrotrophic bacterium applicable in species  
XX -specific detection of the microorganism as indication in studying and  
XX monitoring its growth and circulation of deep-sea water with sensitivity.  
XX Claim 1; Page 30; 37pp; Japanese.  
XX  
XX The invention relates to a 1526 bp Psychrobacter pacificensis 16S rDNA  
XX sequence (AAC87531) and an oligonucleotide probe (AAC87532) comprising  
XX part of the Psychrobacter pacificensis 16S rDNA sequence which are used  
XX for monitoring the growth of psychrophilic bacteria and the circulation  
XX of deep-sea water. Psychrobacter pacificensis is an aerobic, Gram-  
XX negative, non-motile, non-spore-forming oxidase-positive bacterium

CC originally isolated from the Japan Trench. The invention also relates to  
CC a novel method for detecting or specifically identifying *Psychrobacter*  
CC *pacificensis*, *Psychrobacter* glaciicola, and related species, or  
CC *Psychrobacter* pacificensis only via the use of the 16S rDNA sequence. The  
CC 16S rDNA sequence and derived oligonucleotide probe are useful for the  
CC species-specific detection of *Psychrobacter* pacificensis to study and  
CC monitor its growth as an indicator of the circulation of deep-sea water.  
CC The method of the invention is rapid, accurate and has high sensitivity,  
CC and removes the need to separate and culture the biological materials.  
CC The present sequence represents the *Psychrobacter* pacificensis 16S rDNA  
XX  
SQ Sequence 1526 BP; 401 A; 332 C; 467 G; 323 T; 0 U; 3 Other;

Query Match 100.0%; Score 1526; DB 4; Length 1526;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTTGATCATGGCTCCAGATTGAACGACTGGCGGCGAGGCTTAACACATGCAAGTCGAGCG 60  
Db 1 TTTGATCATGGCTCCAGATTGAACGACTGGCGGCGAGGCTTAACACATGCAAGTCGAGCG 60

Qy 61 GAAACGATGATAGCTTCTATTAGGCTCGAGNCGCGGAGTGAATTAATCTTAGGA 120  
Db 61 GAAACGATGATAGCTTCTATTAGGCTCGAGNCGCGGAGTGAATTAATCTTAGGA 120

Qy 121 ATCTACCTAGTAGTGGGGATAGCTCGGGGAACTCGAATTAATACCGCATAGCTACG 180  
Db 121 ATCTACCTAGTAGTGGGGATAGCTCGGGGAACTCGAATTAATACCGCATAGCTACG 180

Qy 181 GGAGAAAGAGGGGNTCAATAGACCTTCGCTTATAGATGAGCTAAGTCGGATTAGCTA 240  
Db 181 GGAGAAAGAGGGGNTCAATAGACCTTCGCTTATAGATGAGCTAAGTCGGATTAGCTA 240

Qy 241 GATGGTGGGTAAGGCTTACCATTGGCGACGATCTGTAGCTGTCTGAGAGGATGATCAG 300  
Db 241 GATGGTGGGTAAGGCTTACCATTGGCGACGATCTGTAGCTGTCTGAGAGGATGATCAG 300

Qy 301 CCACACGGGACTGAGACACGGCCCGGACTCTACGGAGGACGAGTGGGGATATTGGA 360  
Db 301 CCACACGGGACTGAGACACGGCCCGGACTCTACGGAGGACGAGTGGGGATATTGGA 360

Qy 361 CAATGNGGGAACCTCTATCCAGCATCGCGGTGTGGAAGAGGCTTTTGGTGTAA 420  
Db 361 CAATGNGGGAACCTCTATCCAGCATCGCGGTGTGGAAGAGGCTTTTGGTGTAA 420

Qy 421 AGCACTTTAAGCAGTGAAGAAGACTCTTCGGTTAATACCGGGGACGATGACATAGCTG 480  
Db 421 AGCACTTTAAGCAGTGAAGAAGACTCTTCGGTTAATACCGGGGACGATGACATAGCTG 480

Qy 481 CAGNATTAAGCACCGGCTAACTCTGTGCGAGGCGCGGTAAATACAGAGGGTCCAGCGT 540  
Db 481 CAGNATTAAGCACCGGCTAACTCTGTGCGAGGCGCGGTAAATACAGAGGGTCCAGCGT 540

Qy 541 TAATCGGAATTTACTGGCGGTAAAGCGAGCTAGTGGCTTGTATAGTCAGATGTGAATC 600  
Db 541 TAATCGGAATTTACTGGCGGTAAAGCGAGCTAGTGGCTTGTATAGTCAGATGTGAATC 600

Qy 601 CCCGGGCTTAACCTGGGAACCTGCTGAACTCTGTTAGGCTAGAGTAGGTGAGAGGGAAG 660  
Db 601 CCCGGGCTTAACCTGGGAACCTGCTGAACTCTGTTAGGCTAGAGTAGGTGAGAGGGAAG 660

Qy 661 TAGAATTTCAAGTGTAGCGGTGAATCGTAGAGATCTGAAGGAATACCGATGCGGAAG 720  
Db 661 TAGAATTTCAAGTGTAGCGGTGAATCGTAGAGATCTGAAGGAATACCGATGCGGAAG 720

Qy 721 CAGCTTCCTGGCATCATCTGACACTGAGGCTCGAAAGCGTGGGTAGCAACAGGATTAG 780  
Db 721 CAGCTTCCTGGCATCATCTGACACTGAGGCTCGAAAGCGTGGGTAGCAACAGGATTAG 780

Qy 781 ATACCCCTGGTAGTCCACCGCGTAAACGATGCTACTAGTCTGTGGGTCCCTTGAGGACTT 840  
Db 781 ATACCCCTGGTAGTCCACCGCGTAAACGATGCTACTAGTCTGTGGGTCCCTTGAGGACTT 840

Qy 841 AGTGACGCGAGCTAACCAATAAGTACAGCGCTGGGAGTACGCGCGAAGGTATAAAT 900  
Db 841 AGTGACGCGAGCTAACCAATAAGTACAGCGCTGGGAGTACGCGCGAAGGTATAAAT 900

Qy 901 CAAATGAATTTGACGGGGGCGGCACAAAGCGGTGGAGCATGTGTTTAATTCGATGCAACG 960  
Db 901 CAAATGAATTTGACGGGGGCGGCACAAAGCGGTGGAGCATGTGTTTAATTCGATGCAACG 960

Qy 961 CGAAGAACCTTACCTGCTTGTGATACACAGAACTCTTGTAGAGATACGAGATGCGCTTC 1020  
Db 961 CGAAGAACCTTACCTGCTTGTGATACACAGAACTCTTGTAGAGATACGAGATGCGCTTC 1020

Qy 1021 GGGAAATTGTGATACAGGTGCTGATGGCTGCTCGTCAAGTCTGTCGTGAGATGTTGGTT 1080  
Db 1021 GGGAAATTGTGATACAGGTGCTGATGGCTGCTCGTCAAGTCTGTCGTGAGATGTTGGTT 1080

Qy 1081 AAGTCCCGCAACGAGCGCAACCCCTTCTTCTAGTTTACAGCACTTCGGGTGGAACTCTA 1140  
Db 1081 AAGTCCCGCAACGAGCGCAACCCCTTCTTCTAGTTTACAGCACTTCGGGTGGAACTCTA 1140

Qy 1141 AGGATATGCGCAGTGACAAACTGGAGGAAGCGGGAGCGACGTCAGTCAATCATGSCCT 1200  
Db 1141 AGGATATGCGCAGTGACAAACTGGAGGAAGCGGGAGCGACGTCAGTCAATCATGSCCT 1200

Qy 1201 TAGCACCAGGCTTACACAGCTGCTCAATGTTAGTACAGAGGCGAGCTACACAGCGATG 1260  
Db 1201 TAGCACCAGGCTTACACAGCTGCTCAATGTTAGTACAGAGGCGAGCTACACAGCGATG 1260

Qy 1261 TGATGGAATCTCAAAAGGCTATCTGATGTCAGATTTGGAGTCTGCAACTCGACTCCATG 1320  
Db 1261 TGATGGAATCTCAAAAGGCTATCTGATGTCAGATTTGGAGTCTGCAACTCGACTCCATG 1320

Qy 1321 AAGTAGAATCGTGTAGTAACTCGCGGATCAGAAATCGCGGTGAATAGCTTCCCGGGCTT 1380  
Db 1321 AAGTAGAATCGTGTAGTAACTCGCGGATCAGAAATCGCGGTGAATAGCTTCCCGGGCTT 1380

Qy 1381 GTACACACCGCGCTCACACCTGGGAGTTGATTGCACCAAGAGTGGTTAGCCCTAACTTA 1440  
Db 1381 GTACACACCGCGCTCACACCTGGGAGTTGATTGCACCAAGAGTGGTTAGCCCTAACTTA 1440

Qy 1441 GTGAGGCGGATCACACCGGTGCTGATGATCGAGTGAAGTGGGTGAAGTGAAGTGGCGT 1500  
Db 1441 GTGAGGCGGATCACACCGGTGCTGATGATCGAGTGAAGTGGGTGAAGTGAAGTGGCGT 1500

Qy 1501 AGGGGAACCTGCGGCTGGATCACCTC 1526  
Db 1501 AGGGGAACCTGCGGCTGGATCACCTC 1526

## RESULT 2

AAQ13256  
ID AAQ13256 standard; DNA; 1485 BP.

XX AAQ13256;

XX AC AC

XX 24-OCT-2003 (revised)

XX 25-MAR-2003 (revised)

XX 25-OCT-1991 (first entry)

XX DE DE

XX 16S rRNA gene (partial).

XX KW KW

XX Probe; detection; Moraxella; Neisseria; 23S; ribosomal RNA; ss.

XX OS OS

XX Moraxella catarrhalis; ITG 4197.

XX PN PN

XX WO9111531-A.

XX PD PD

XX 08-AUG-1991.

XX XX

XX 02-FEB-1990; 90EP-00400297.

XX PR PR

XX 02-FEB-1990; 90EP-00400297.

•

CC associated with flea infestations. For example, the nucleic acids may be  
 CC used to produce an HMT or HNC protein according to standard recombinant  
 CC DNA methodology by inserting the nucleic acids into a host cell and  
 CC culturing the cell to express the protein. The HMT and HNC nucleic acids  
 CC may also be used as DNA probes in diagnostic assays (e.g., PCR) to detect  
 CC and quantitate the presence of cat flea or other homologous nucleic acid  
 CC sequences in samples. They may also be used to study the expression and  
 CC function of the proteins and their role in metabolism. The HMT and HNC  
 CC proteins may be used as antigens in the production of specific  
 CC antibodies, and in assays to identify modulators (agonists and  
 CC antagonists) of HMT and/or HNC protein expression and activity. The anti-  
 CC HMT/HNC protein antibodies and antagonists may also be used to  
 CC downregulate protein expression and activity. The antibodies may also be  
 CC used as diagnostic agents for detecting the presence of flea polypeptides  
 CC in samples (e.g., by enzyme linked immunosorbent assay (ELISA)). The  
 CC present sequence represents a cat flea HNC cDNA of the invention  
 XX  
 SQ Sequence 549 BP; 132 A; 131 C; 173 G; 112 T; 0 U; 1 Other;

Query Match 7.9%; Score 121; DB 3; Length 549;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-52;  
 Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 866 GACGCGCTGGGAGTACGGCGCAAGGTTAAACTCAAAATGAATTGACGGGGGCCGCGAC 925  
 DB 163 GACGCGCTGGGAGTACGGCGCAAGGTTAAACTCAAAATGAATTGACGGGGGCCGCGAC 222  
 QY 926 AAGCGGTGGAGCATGTGGTTTAATTCGATGCAACGGCGAAGAACCTTACCTGGTCTTGACA 985  
 DB 223 AAGCGGTGGAGCATGTGGTTTAATTCGATGCAACGGCGAAGAACCTTACCTGGTCTTGACA 282  
 QY 986 T 986  
 DB 283 T 283

RESULT 5  
 AAS11034  
 ID AAS11034 standard; DNA; 1487 BP.  
 XX AC AAS11034;  
 XX AC AAS11034;  
 DT 06-AUG-2003 (revised)  
 DT 24-OCT-2001 (first entry)  
 XX Shigella dysenteriae 16s ribosomal RNA gene.  
 XX Antisense; bacterial 16s ribosomal RNA; rRNA; bacterial infection; human;  
 KW food grain supplement; livestock; poultry; therapeutic; ds.  
 XX Shigella dysenteriae.  
 XX WO200142457-A2.  
 XX 14-JUN-2001.  
 XX 29-NOV-2000; 2000WO-US042391.  
 PF 29-NOV-1999; 99US-0168150P.  
 PR (AVIB-) AVI BIOPHARMA INC.  
 XX Iversen PL;  
 XX WPI; 2001-457295/49.  
 XX Antibacterial compound, useful for treating bacterial infections and as  
 PT livestock and poultry food supplement, comprises antisense  
 PT oligonucleotides complementary to bacterial 16S and 23S rRNA.  
 XX  
 PS Disclosure; Page: 62pp; English.  
 XX AAS11021-AAS11034 represent the coding sequences of bacterial 16s

CC ribosomal RNA (rRNA) genes. The sequences were used to design anti-  
 CC bacterial compounds comprising substantially uncharged antisense  
 CC oligomers containing 8-40 nucleotide subunits, including a targeting  
 CC nucleic acid sequence at least 10 nucleotides in length which is  
 CC complementary to a bacterial 16S or 23S rRNA nucleic acid sequence. The  
 CC antisense oligomers are used for treating a bacterial infection in a  
 CC human or a mammalian animal produced by *Escherichia coli*, *Salmonella*  
 CC typhimurium, *Pseudomonas aeruginosa*, *Vibrio cholera*, *Neisseria*  
 CC gonorrhoea, *Helicobacter pylori*, *Bartonella henselae*, *Haemophilus*  
 CC influenza, *Shigella dysenteriae*, *Staphylococcus aureus*, *Mycobacterium*  
 CC tuberculosis, *Streptococcus pneumoniae*, *Treponema pallidum* and *Chlamydia*  
 CC trachomatis. The antibacterial compound may be used as a food grain  
 CC supplement in livestock and poultry food composition. Note: The present  
 CC sequence is not shown in the specification but has been accessed from  
 CC GenBank using the appropriate accession number given in the  
 CC specification. (Updated on 06-AUG-2003 to correct OS field.)  
 XX  
 SQ Sequence 1487 BP; 375 A; 341 C; 472 G; 299 T; 0 U; 0 Other;

Query Match 7.9%; Score 121; DB 5; Length 1487;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-52;  
 Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 866 GACGCGCTGGGAGTACGGCGCAAGGTTAAACTCAAAATGAATTGACGGGGGCCGCGAC 925  
 DB 857 GACGCGCTGGGAGTACGGCGCAAGGTTAAACTCAAAATGAATTGACGGGGGCCGCGAC 916  
 QY 926 AAGCGGTGGAGCATGTGGTTTAATTCGATGCAACGGCGAAGAACCTTACCTGGTCTTGACA 985  
 DB 917 AAGCGGTGGAGCATGTGGTTTAATTCGATGCAACGGCGAAGAACCTTACCTGGTCTTGACA 976  
 QY 986 T 986  
 DB 977 T 977

RESULT 6  
 ABS71622  
 ID ABS71622 standard; DNA; 1489 BP.  
 XX AC ABS71622;  
 XX AC ABS71622;  
 DT 28-NOV-2002 (first entry)  
 DT Klebsiella pneumoniae 16S RNA.  
 DE Klebsiella pneumoniae.  
 KW Rubacteria; species detection; speciation; 16s RNA; gene; ss.  
 XX Klebsiella pneumoniae.  
 OS WO200270728-A2.  
 XX 12-SEP-2002.  
 XX 01-MAR-2002; 2002WO-US060650.  
 XX 01-MAR-2001; 2001US-0272642P.  
 XX (UJJO ) UNIV JOHNS HOPKINS.  
 XX Rothman RE, Yang S, Lin S, Kelen GD;  
 WPI; 2002-698755/75.  
 XX Detecting and determining species source of eubacterial DNA in a sample,  
 PT comprises amplifying template DNA in the sample using a real-time  
 PT polymerase chain reaction with the use of primers and at least two  
 PT fluorogenic probes.  
 XX Example 1; Page: 39pp; English.  
 XX The invention describes a method of detecting and determining species  
 CC source of eubacterial DNA in a sample. The method comprises amplifying

CC template DNA in the sample using a real-time polymerase chain reaction (R  
-T PCR), where the PCR or PCR reaction mixture comprises primers and at  
CC least two fluorogenic probes. The methods are useful in detecting and  
CC determining species source of eubacterial DNA in a sample. The present  
CC method allows for highly sensitive detection of any eubacterial species  
CC with simultaneous speciation. It eliminates false positive results in  
CC detecting bacterial infections. This sequence represents a bacterial 16S  
CC RNA gene used to create the primers of the invention

XX SQ Sequence 1489 BP; 375 A; 341 C; 475 G; 294 T; 0 U; 4 Other;

Query Match 7.9%; Score 121; DB 6; Length 1489;  
Best Local Similarity 100.0%; Pred. No. 1.8e-52;  
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 866 GACCGCTGGGAGTACGCCCAAGGTTAAACTCAAATGAATTGACGGGGCCCGCAC 925  
DB 846 GACCGCTGGGAGTACGCCCAAGGTTAAACTCAAATGAATTGACGGGGCCCGCAC 905  
QY 926 AAGCGTGGAGCATGTGTTTAAATTCGATGCAACCGAAGAACCTTACTGCTTTGACA 985  
DB 906 AAGCGTGGAGCATGTGTTTAAATTCGATGCAACCGAAGAACCTTACTGCTTTGACA 965  
QY 986 T 986  
DB 966 T 966

## RESULT 7

ABST71613  
ID ABS71613 standard; DNA; 1506 BP.

XX AC ABS71613;

DT 28-NOV-2002 (first entry)

XX DE Escherichia coli 16S RNA.

XX KW Eubacteria; species detection; speciation; 16S RNA; gene; ss.

XX OS Escherichia coli;

XX PN WO200270728-A2.

XX PD 12-SEP-2002.

XX PF 01-MAR-2002; 2002WO-US006050.

XX PR 01-MAR-2001; 2001US-0272642P.

XX PA (UYJO ) UNIV JOHNS HOPKINS.

XX PI Rothman RE, Yang S, Lin S, Kelen GD;

XX DR WPI; 2002-698755/75.

XX PT Detecting and determining species source of eubacterial DNA in a sample,  
XX comprises amplifying template DNA in the sample using a real-time  
PT polymerase chain reaction with the use of primers and at least two  
PT fluorogenic probes.

XX FS Example 1; Page; 39pp; English.

XX The invention describes a method of detecting and determining species  
CC source of eubacterial DNA in a sample. The method comprises amplifying  
CC template DNA in the sample using a real-time polymerase chain reaction (R  
-T PCR), where the PCR or PCR reaction mixture comprises primers and at  
CC least two fluorogenic probes. The methods are useful in detecting and  
CC determining species source of eubacterial DNA in a sample. The present  
CC method allows for highly sensitive detection of any eubacterial species  
CC with simultaneous speciation. It eliminates false positive results in  
CC detecting bacterial infections. This sequence represents a bacterial 16S  
CC RNA gene used to create the primers of the invention

XX SQ Sequence 1506 BP; 378 A; 346 C; 481 G; 301 T; 0 U; 0 Other;

Query Match 7.9%; Score 121; DB 6; Length 1506;  
Best Local Similarity 100.0%; Pred. No. 1.8e-52;  
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 866 GACCGCTGGGAGTACGCCCAAGGTTAAACTCAAATGAATTGACGGGGCCCGCAC 925  
DB 857 GACCGCTGGGAGTACGCCCAAGGTTAAACTCAAATGAATTGACGGGGCCCGCAC 916

QY 926 AAGCGTGGAGCATGTGTTTAAATTCGATGCAACCGAAGAACCTTACTGCTTTGACA 985  
DB 917 AAGCGTGGAGCATGTGTTTAAATTCGATGCAACCGAAGAACCTTACTGCTTTGACA 976

QY 986 T 986

DB 977 T 977

## RESULT 8

ADQ81656  
ID ADQ81656 standard; DNA; 1533 BP.

XX AC ADQ81656;

XX DT 21-OCT-2004 (first entry)

XX DE Enterobacter sp. C-1 strain 16S rRNA gene SeqID 1.

XX KW microorganism; 16S rRNA; ds; water soluble polysaccharide; fucose;  
XX galactose; glucose; glucuronic acid; anti-cancer;  
XX 4,5-dihydroxy 2-cyclopentene-1-one; DHCP; food; paper diaper.

XX OS Enterobacter sp.

XX PN JP2004208563-A.

XX PD 29-JUL-2004.

XX PF 27-DEC-2002; 2002JP-00380990.

XX PR 27-DEC-2002; 2002JP-00380990.

XX PA (ASAH ) ASahi KASEI KK.

XX DR WPI; 2004-538189/52.

XX PT Novel microorganism having 16S rRNA gene, useful for producing water-  
PT soluble polysaccharide which produces anti-cancer substance on heating  
PT for long time.

XX FS Claim 1; SEQ ID NO 1; 15pp; Japanese.

XX This invention relates to a novel microorganism having a 16S rRNA gene  
CC comprising a fully defined sequence of 1533 nucleotides. Specifically, it  
CC refers to a water soluble polysaccharide producing microbe identified as  
CC Enterobacter sp. C-1 (FERM P-18947). The present invention describes the  
CC water soluble polysaccharide as comprising fucose, galactose, glucose and  
CC glucuronic acid, and collection of the same involves altering the pH  
CC value of the microbial culture solution to pH 4 by adding long-chain  
CC quaternary ammonium salt in order to isolate the ammonium salt  
CC precipitate of the polysaccharide. Accordingly, this microorganism is  
CC useful for producing water-soluble polysaccharides that in turn can be  
CC used to produce the anti-cancer substance 4,5-dihydroxy 2-cyclopentene-1-  
CC one (DHCP). Furthermore, the water-soluble polysaccharide compositions  
CC are useful in food and paper diaper products. This polynucleotide  
CC sequence is the Enterobacter sp. C-1 strain 16S rRNA gene of the  
CC invention.

XX SQ Sequence 1533 BP; 383 A; 354 C; 489 G; 307 T; 0 U; 0 Other;

Query Match 7.9%; Score 121; DB 13; Length 1533;



Query Match 7.9%; Score 121; DB 1; Length 1540;  
 Best Local Similarity 80.2%; Pred. No. 1.8e-52;  
 Matches 97; Conservative 24; Mismatches 0; Indels 0; Gaps 0;

QY 866 GACCGCTGGGAGTACGCCGCAAGTTTAAATCGATGCAACGCGAAGAACCTTACCTGGTCTTGACA 925  
 DB 876 GACCGCTGGGAGTACGCCGCAAGTTTAAATCGATGCAACGCGAAGAACCTTACCTGGTCTTGACA 935

QY 926 AAGCGGTGGAGCATGTGTTTAAATCGATGCAACGCGAAGAACCTTACCTGGTCTTGACA 985  
 DB 936 AAGCGGTGGAGCATGTGTTTAAATCGATGCAACGCGAAGAACCTTACCTGGTCTTGACA 995

QY 986 T 986  
 DB 996 U 996

RESULT 11  
 AAT29140  
 ID AAT29140 standard; DNA; 1542 BP.  
 AC AAT29140;  
 XX  
 DT 02-DEC-1996 (first entry)  
 XX  
 DE rRNA gene (rrsE) from *Escherichia coli*.  
 XX  
 KW p53; mutant; mutation; cleavage; nuclease; cleavage; Thermus;  
 KW *Escherichia*; *Saccharomyces*; *Campylobacter*; *Mycobacterium*; *Shigella*;  
 KW *Staphylococcus*; identification; detection; ds.  
 XX  
 OS *Escherichia coli*.  
 XX  
 PN WO9615267-A1.  
 XX  
 PD 23-MAY-1996.  
 XX  
 PF 09-NOV-1995; 95WO-US014673.  
 XX  
 PR 09-NOV-1994; 94US-00337164.  
 PR 09-MAR-1995; 95US-00402601.  
 PR 07-JUN-1995; 95US-00484956.  
 PR 30-AUG-1995; 95US-00520946.  
 XX  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 XX  
 PI Dahlberg JE, Lyamichev VI, Brow MAD, Oldenburg MC, Heisler LM;  
 PI Fors L, Olive DW;  
 XX  
 DR WPI; 1996-259862/26.  
 XX  
 PT Cleavage of nucleic acids to detect mutation(s) - allows detection esp.  
 PT in human p53 gene, to identify strains of microorganisms and viruses.  
 XX  
 PS Example 34; Page 314; 433pp; English.  
 XX  
 CC Cleavage of nucleic acids using an enzyme, especially a nuclease selected  
 CC from the group consisting of cleavage (RTM) BN enzyme, *Thermus aquaticus*  
 CC DNA polymerase, *Thermus thermophilus* DNA polymerase, *Escherichia coli*  
 CC ExoII and the *Saccharomyces cerevisiae* Radi/Rad10 complex. The nucleic  
 CC acid substrate is preferably an oligonucleotide containing a human p53  
 CC gene sequence or alternatively, microbial gene sequences. Cleavage  
 CC products are compared to the cleavage products of reference gene  
 CC sequences. The method is used for detecting mutation in the human p53  
 CC gene; for identifying strains of microorganisms, especially bacteria  
 CC selected from the group of members of the genera *Campylobacter*,  
 CC *Escherichia*, *Mycobacterium*, *Salmonella*, *Shigella* and *Staphylococcus*. The  
 CC method may also be used for the identification of viruses, especially  
 CC hepatitis C virus (HCV) and simian immunodeficiency virus (SIV). Seven  
 CC primers (AAT29133-39) were used to amplify 16S rRNA genes. The amplified  
 CC genes were then subjected to the cleavage method and the resulting  
 CC fragmentation patterns used in identification of the microorganisms from

CC which the rRNA genes originated. 16S rRNA genes are given in AAT29140-42  
 XX Sequence 1542 BP; 389 A; 352 C; 487 G; 314 T; 0 U; 0 Other;  
 SQ

Query Match 7.9%; Score 121; DB 2; Length 1542;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-52;  
 Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 866 GACCGCTGGGAGTACGCCGCAAGTTTAAATCGATGCAACGCGGCGCCGCGAC 925  
 DB 877 GACCGCTGGGAGTACGCCGCAAGTTTAAATCGATGCAACGCGGCGCCGCGAC 936

QY 926 AAGCGGTGGAGCATGTGTTTAAATCGATGCAACGCGGAAACCTTACCTGGTCTTGACA 985  
 DB 937 AAGCGGTGGAGCATGTGTTTAAATCGATGCAACGCGGAAACCTTACCTGGTCTTGACA 996

QY 986 T 986  
 DB 997 T 997

RESULT 12  
 AAC62270  
 ID AAC62270 standard; DNA; 1542 BP.  
 AC AAC62270;  
 XX  
 DT 19-MAR-2001 (first entry)  
 XX  
 DE *Escherichia coli* reference 16S rDNA sequence.  
 XX  
 KW 16S rDNA; dechlorinating activity; chlorinated compound; vinyl chloride;  
 KW carbontetrachloride; tetrachloroethane; chloroform; dichloromethane;  
 KW trichloroethane; dichloroethylene; chlorinating bacteria; ss.  
 XX  
 OS *Escherichia coli*.  
 XX  
 PN WO200063443-A2.  
 XX  
 PD 26-OCT-2000.  
 XX  
 PF 13-APR-2000; 2000WO-US009883.  
 XX  
 PR 15-APR-1999; 99US-0129511P.  
 XX  
 PA (DUPO) DU PONT DE NEMOURS & CO E I.  
 XX  
 PI Hendrickson ER, Ebersole RC;  
 XX  
 DR WPI; 2001-024581/03.  
 XX  
 PT New 16S rDNA profile derived from Dehalococcoides ethenogenes and  
 PT indicative of a dechlorinating bacterial strain.  
 XX  
 PS Disclosure; Page 55; 55pp; English.  
 XX  
 CC The present sequence represents a reference 16S rDNA sequence. The  
 CC specification describes 16S rDNA sequences, derived from various strains  
 CC of Dehalococcoides ethenogenes. These 16S rDNA profile is linked to  
 CC dechlorinating activity. Bacterial strain comprising the 16S rDNA  
 CC sequence of the invention are useful for the dechlorination of  
 CC chlorinated compounds such as carbontetrachloride, tetrachloroethane,  
 CC chloroform, dichloromethane, trichloroethane, dichloroethylene, vinyl  
 CC chloride, and chloroformatics. The 16S rDNA sequence is also useful for  
 CC identification of new chlorinating bacteria, as well as sub-typing  
 CC strains of Dehalococcoides ethenogenes  
 XX  
 SQ Sequence 1542 BP; 389 A; 352 C; 487 G; 314 T; 0 U; 0 Other;  
 XX

Query Match 7.9%; Score 121; DB 4; Length 1542;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-52;  
 Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 866 GACCGCTGGGAGTACGGCCGCAAGGTTAAACTCAATGATTGACGGGGCCGCGAC 925
DB 877 GACCGCTGGGAGTACGGCCGCAAGGTTAAACTCAATGATTGACGGGGCCGCGAC 936
QY 926 AAGCGGTGGAGCATGTGGTTTAATTCGATCGAACGCGAAGAACCTTACCTGCTTTGACA 985
DB 937 AAGCGGTGGAGCATGTGGTTTAATTCGATCGAACGCGAAGAACCTTACCTGCTTTGACA 996
QY 986 T 986
DB 997 T 997

RESULT 13
ID AAF23015 standard; rRNA; 1542 BP.
XX
AC AAF23015;
XX
DT 20-MAR-2001 (first entry)
XX
DE E. coli 16S rRNA sequence.
XX
KW Probe; PCR primer; 5S rRNA; 16S rRNA; 23S rRNA; 28S rRNA; 18S rRNA;
KW Mycobacterium; Enterococcus; Chlamydia; Mycoplasma; E. coli; Legionella;
KW Salmonella; Pseudomonas; Campylobacter; Neisseria gonorrhoeae; fungus;
KW Bacterium; ss.
XX
OS Escherichia coli.
XX
PN US6150517-A.
XX
PD 21-NOV-2000.
XX
PF 30-MAY-1995; 95US-00454063.
XX
PR 24-NOV-1986; 86US-00934244.
PR 07-AUG-1987; 87US-00083542.
PR 24-NOV-1987; 87WO-US003009.
PR 09-DEC-1988; 88US-00295208.
PR 11-DEC-1991; 91US-00806929.
PR 22-FEB-1994; 94US-00200866.
XX
PA (GENP-) GEN-PROBE INC.
XX
PI McDonough SH, Kop JA, Smith RD, Hogan JJ;
XX
DR WPI; 2001-060029/07.
XX
PT Preparing a probe for nucleic acid hybridization assays comprises
PT constructing a nucleotide polymer sufficiently complementary to hybridize
PT to an rRNA region that distinguishes non-viral target from non-viral non-
PT target species.
XX
PS Disclosure; Fig 1; 75pp; English.
XX
CC The present invention provides novel methods of producing probes for use
CC in the identification of a number of microorganisms. These include E.
CC coli, Mycobacteria, Mycoplasma, Campylobacter, Chlamydia, Enterobacter,
CC Legionella, Salmonella, Pseudomonas, Neisseria gonorrhoeae, fungi and
CC bacteria
XX
SQ Sequence 1542 BP; 389 A; 351 C; 488 G; 0 T; 314 U; 0 Other;
Query Match 7.9%; Score 121; DB 5; Length 1542;
Best Local Similarity 80.2%; Pred. No. 1.8e-52;
Matches 97; Conservative 24; Mismatches 0; Indels 0; Gaps 0;

QY 866 GACCGCTGGGAGTACGGCCGCAAGGTTAAACTCAATGATTGACGGGGCCGCGAC 925
DB 877 GACCGCTGGGAGTACGGCCGCAAGGTTAAACTCAATGATTGACGGGGCCGCGAC 936
QY 926 AAGCGGTGGAGCATGTGGTTTAATTCGATCGAACGCGAAGAACCTTACCTGCTTTGACA 985
DB 937 AAGCGGTGGAGCATGTGGTTTAATTCGATCGAACGCGAAGAACCTTACCTGCTTTGACA 996
QY 986 T 986
DB 997 T 997

RESULT 14
AAH75410
ID AAH75410 standard; rRNA; 1542 BP.
XX
AC AAH75410;
XX
DT 18-OCT-2001 (first entry)
XX
DE E. coli 16S rRNA.
XX
KW 16S rRNA; 23S rRNA; RNA binding; antimicrobial; ss.
XX
OS Escherichia coli.
XX
FH Key Location/Qualifiers
FT misc_binding 9..13
FT /tag= a
FT /bound_moiety= "16S rRNA"
FT /note= "Binds nucleotides 25-21 to form a duplex"
FT misc_binding 17..19
FT /tag= b
FT /bound_moiety= "16S rRNA"
FT /note= "Binds nucleotides 918-916 to form a duplex"
FT misc_binding 21..25
FT /tag= c
FT /bound_moiety= "16S rRNA"
FT /note= "Binds nucleotides 13-9 to form a duplex"
FT misc_binding 27..37
FT /tag= d
FT /bound_moiety= "16S rRNA"
FT /note= "Binds nucleotides 556-547 to form a duplex"
FT misc_binding 39..46
FT /tag= e
FT /bound_moiety= "16S rRNA"
FT /note= "Binds nucleotides 403-394 to form a duplex"
FT misc_binding 52..58
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FT /bound_moiety= "16S rRNA"
FT /note= "Binds nucleotides 359-354 to form a duplex"
FT stem_loop 61..106
FT /tag= g
FT misc_binding 113..115
FT /tag= h
FT /bound_moiety= "16S rRNA"
FT /note= "Binds nucleotides 314-312 to form a duplex"
FT misc_binding 123..142
FT /tag= i
FT /bound_moiety= "16S rRNA"
FT /note= "Binds nucleotides 238-221 to form a duplex"
FT stem_loop 144..178
FT /tag= j
FT stem_loop 184..193
FT /tag= k
FT stem_loop 199..218
FT /tag= l
FT misc_binding 221..238
FT /tag= m
FT /bound_moiety= "16S rRNA"
FT /note= "Binds nucleotides 142-123 to form a duplex"
FT stem_loop 240..286
FT /tag= n
FT stem_loop 289..311
FT /tag= o
FT misc_binding 312..314
FT /tag= p

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FT /bound_moiety= "16S rRNA"
FT /note= "Binds nucleotides 115-113 to form a duplex"
FT stem_loop 316..337
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FT stem_loop 339..350
FT /tag= r
FT misc_binding 354..359
FT /tag= s
FT /bound_moiety= "16S rRNA"
FT /note= "Binds nucleotides 58-52 to form a duplex"
FT stem_loop 367..392
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FT misc_binding 394..403
FT /tag= u
FT /bound_moiety= "16S rRNA"
FT /note= "Binds nucleotides 46-39 to form a duplex"
FT stem_loop 406...436
FT /tag= v
FT stem_loop 442..492
FT /tag= w
FT stem_loop 500..545
FT /tag= x
FT protein_bind 523
FT /tag= y
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FT misc_binding 547..556
FT /tag= z
FT /bound_moiety= "16S rRNA"
FT /note= "Binds nucleotides 37-27 to form a duplex"
FT misc_binding 567..569
FT /tag= aa
FT /bound_moiety= "16S rRNA"
FT /note= "Binds nucleotides 883-881 to form a duplex"
FT misc_binding 577..586
FT /tag= ab
FT /bound_moiety= "16S rRNA"
FT /note= "Binds nucleotides 764-755 to form a duplex"
FT stem_loop 588..651
FT /tag= ac
FT misc_binding 655..671
FT /tag= ad
FT /bound_moiety= "16S rRNA"
FT /note= "Binds nucleotides 751-735 to form a duplex"
FT stem_loop 672..717
FT /tag= ae
FT protein_bind 693
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FT /bound_moiety= "Pactamycin, Edeine"
FT stem_loop 725..732
FT /tag= ag
FT misc_binding 735..751
FT /tag= ah
FT /bound_moiety= "16S rRNA"
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FT misc_binding 755..764
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FT protein_bind 794
FT /tag= ak
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FT /bound_moiety= "Kasugamycin, Pactamycin, Edeine"
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FT stem_loop 861..868

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FT /bound_moiety= "Oxazolidinone"
FT misc_binding 874..879
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FT /bound_moiety= "16S rRNA"
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FT misc_binding 881..883
FT /tag= ar
FT /bound_moiety= "16S rRNA"
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FT stem_loop 885..912
FT /tag= as
FT protein_bind 910
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FT protein_bind 911
FT /tag= au
FT /bound_moiety= "Streptomycin"
FT protein_bind 913
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FT protein_bind 914
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FT protein_bind 915
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FT misc_binding 916..918
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FT /note= "Binds nucleotides 19-17 to form a duplex"
FT misc_binding 921..933
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FT /bound_moiety= "16S rRNA"
FT /note= "Binds nucleotides 1396-1384 to form a duplex"
FT protein_bind 926
FT /tag= ba
FT /bound_moiety= "Kasugamycin, Edeine"
FT misc_binding 938..943
FT /tag= bb
FT /bound_moiety= "16S rRNA"
FT /note= "Binds nucleotides 1345-1340 to form a duplex"
FT misc_binding 946..955
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FT /bound_moiety= "16S rRNA"
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FT stem_loop 960..975
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FT misc_binding 984..990
FT /tag= be
FT /bound_moiety= "16S rRNA"
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FT misc_binding 997..1003
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FT /bound_moiety= "16S rRNA"
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FT stem_loop 1007..1022
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FT stem_loop 1025..1036
FT /tag= bh
FT misc_binding 1037..1044
FT /tag= bi

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Query Match 7.9%; Score 121; DB 5; Length 1542;

~ Best Local Similarity 80.2%; Pred. No. 1.8e-52;

Matches 97; Conservative 24; Mismatches 0; Indels 0; Gaps 0;

Qy 866 GACCGCTGGGGAGTACGGCGCAAGTTAAACTCAATGATTAATGACGGGGCCCGCAC 925

Db 877 GACCGCTGGGGAGTACGGCGCAAGTTAAACTCAATGATTAATGACGGGGCCCGCAC 936



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FT 916..918          /*tag= ao
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FT /note="Binds nucleotides 19-17 to form a duplex"
FT 921..933
FT /tag= ap
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FT /bound_moiety= "16S rRNA"
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FT /note="Binds nucleotides 1235-1225 to form a duplex"
FT 960..975
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FT /bound_moiety= "16S rRNA"
FT /note="Binds nucleotides 1221-1215 to form a duplex"
FT 997..1003
FT /tag= au
FT /bound_moiety= "16S rRNA"
FT /note="Binds nucleotides 1044-1037 to form a duplex"
FT 1007..1022
FT /tag= av
FT 1025..1036
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FT 1037..1044
FT /tag= ax
FT /bound_moiety= "16S rRNA"
FT /note="Binds nucleotides 1003-997 to form a duplex"
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FT /note="Binds nucleotides 1210-1192 to form a duplex"
FT 1048..1209
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FT 1068..1073
FT /tag= ba
FT /bound_moiety= "16S rRNA"
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FT /tag= bb
FT 1087..1098
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FT 1102..1107
FT /tag= bd
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FT 1113..1114
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FT /bound_moiety= "16S rRNA"
FT /note="Binds nucleotides 1187-1186 to form a duplex"
FT 1118..1155
FT /tag= bf
FT 1161..1175
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FT 1186..1187
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FT /bound_moiety= "16S rRNA"
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Query Match 7.9%; Score 121; DB 6; Length 1542;  
Best Local Similarity 80.2%; Pred. No. 1.8e-52;  
Matches 97; Conservative 24; Mismatches 0; Indels 0; Gaps 0;

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Qy 866 GACCGCTGGGAGTACCGCGCAAGGTTAAACTCAATGACGGGGCCCGCAC 925
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 877 GACCGCUGGGGAGUACGGCGCAAGGUUAAAAACUCAAUGAAUUGACGGGGCCCGCAC 936
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```
Qy 926 AAGCGTGGAGCATGTGTTTAAATTCGATGCAACGCGAAGACCTTACCTGCTTGACA 985
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 937 AAGCGGUGGAGCAUGUGGUUUAUUCGAUGCAACGCGAAGACCUUACCGGUCUGACA 996

Qy 986 T 986
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Db 997 U 997
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OM nucleic - nucleic search, using sw model

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	136	8.9	1485	1 US-08-299-810A-27	Sequence 27, Appl
2	136	8.9	269223	4 US-09-596-002-41	Sequence 41, Appl
3	121	7.9	881	5 PCT-US91-01574-13	Sequence 13, Appl
4	121	7.9	882	2 US-07-923-871C-13	Sequence 13, Appl
5	121	7.9	1487	4 US-09-726-774-14	Sequence 14, Appl
6	121	7.9	1542	1 US-08-114-695A-1	Sequence 1, Appl
7	121	7.9	1542	2 US-08-757-653-158	Sequence 158, App
8	121	7.9	1542	3 US-09-465-355-2	Sequence 2, Appl
9	121	7.9	1542	4 US-08-520-946-158	Sequence 158, App
10	121	7.9	1542	4 US-09-655-378A-158	Sequence 158, App
11	121	7.9	1542	4 US-09-548-998E-33	Sequence 33, Appl
12	121	7.9	1549	4 US-09-492-709A-89	Sequence 89, Appl
13	121	7.9	1549	4 US-09-492-709A-242	Sequence 242, App
14	121	7.9	1549	4 US-09-492-709A-402	Sequence 402, App
15	114	7.5	1541	4 US-09-726-774-2	Sequence 2, Appl
16	110	7.2	1830121	4 US-09-557-884-1	Sequence 1, Appl
17	110	7.2	1830121	4 US-09-557-884-1	Sequence 1, Appl
18	110	7.2	1830121	4 US-09-643-990A-1	Sequence 1, Appl
19	110	7.2	1830121	4 US-09-643-990A-1	Sequence 1, Appl
20	109	7.1	1506	4 US-10-278-942-1	Sequence 1, Appl
21	97	6.4	140	2 US-08-744-490-8	Sequence 8, Appl
22	97	6.4	140	2 US-08-744-490-10	Sequence 10, Appl
23	97	6.4	140	2 US-08-744-490-11	Sequence 11, Appl
24	97	6.4	140	2 US-08-744-490-12	Sequence 12, Appl
25	97	6.4	140	2 US-08-744-490-13	Sequence 13, Appl
26	97	6.4	140	2 US-08-744-490-14	Sequence 14, Appl
27	88	5.8	1501	4 US-09-793-920A-1	Sequence 1, Appl

28	88	5.8	1501	4 US-09-821-016-5	Sequence 5, Appl
29	88	5.8	1501	4 US-09-745-476-1	Sequence 1, Appl
30	88	5.8	1501	4 US-09-748-205-1	Sequence 1, Appl
31	88	5.8	1501	4 US-09-951-720-1	Sequence 1, Appl
32	88	5.8	1501	4 US-10-411-319-1	Sequence 1, Appl
33	88	5.8	1501	4 US-10-105-305-1	Sequence 1, Appl
34	88	5.8	1501	4 US-10-266-787-5	Sequence 5, Appl
35	84	5.5	1429	4 US-09-934-868-81	Sequence 81, Appl
36	83	5.4	1449	3 US-09-602-417-1	Sequence 1, Appl
37	83	5.4	1451	3 US-09-342-579-1	Sequence 1, Appl
38	83	5.4	1451	3 US-09-617-854A-1	Sequence 1, Appl
39	83	5.4	1474	1 US-08-114-695A-8	Sequence 8, Appl
40	83	5.4	1495	3 US-09-063-898-1	Sequence 1, Appl
41	83	5.4	1495	4 US-09-985-846-1	Sequence 1, Appl
42	83	5.4	1500	4 US-09-726-774-4	Sequence 4, Appl
43	78	5.1	354	4 US-09-328-352-1462	Sequence 1462, Ap
44	77	5.0	1540	3 US-09-228-184-1	Sequence 1, Appl
45	77	5.0	1540	4 US-09-967-376-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1  
US-08-299-810A-27  
; Sequence 27, Application US/08299810A  
; Patent No. 5721097  
; GENERAL INFORMATION:  
; APPLICANT: Rossau, Rudi  
; APPLICANT: Van Heuverswyn, Hugo  
; TITLE OF INVENTION: HYBRIDIZATION PROBES FOR THE  
; DETECTION OF BRANHAMELLA CATARRHALIS STRAINS  
; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Merchant & Gould  
; STREET: 3100 No. 5721097west Center  
; CITY: Minneapolis  
; STATE: MN  
; COUNTRY: USA  
; ZIP: 55402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/299,810A  
; FILING DATE: 01-SEP-1994  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hillson, Randall A.  
; REGISTRATION NUMBER: 31,838  
; REFERENCE/DOCKET NUMBER: 8076.70-US-WO  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 612-332-5300  
; TELEFAX: 612-332-9081  
; INFORMATION FOR SEQ ID NO: 27:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1485 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; ORIGINAL SOURCE:  
; ORGANISM: Branhamella catarrhalis  
; IMMEDIATE SOURCE:  
; CLONE: 16S rRNA Gene  
US-08-299-810A-27

Query Match 8.9%; Score 136; DB 1; Length 1485;  
Best Local Similarity 100.0%; Pred. No. 5.9e-61;  
Matches 136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

852	TAACGCAATAAGTAGACCGCCTGGGAGTACGGCCGCAAGTTAAAACTCAATGAATTG	911
Qy		
809	TAACGCAATAAGTAGACCGCCTGGGAGTACGGCCGCAAGTTAAAACTCAATGAATTG	868
Db		
912	ACGGGGGCCGCACAAAGCGGTGGAGCATGTGTTTAAATTGATGCAACGGCAAGAACCTT	971
Qy		
869	ACGGGGGCCGCACAAAGCGGTGGAGCATGTGTTTAAATTGATGCAACGGCAAGAACCTT	928
Db		
972	ACCTGGTCTTTGACATA	987
Qy		
929	ACCTGGTCTTTGACATA	944
Db		

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RESULT 2
US-09-596-002-41/c
; Sequence 41, Application US/09596002
; Patent No. 6632636
; GENERAL INFORMATION:
; APPLICANT: Lagace, Robert, E.
; APPLICANT: Patterson, Chandra
; APPLICANT: Berg, Kim, L.
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF MORAXELLA CATARRHALIS GENOME
; FILE REFERENCE: PM-0008-4 US
; CURRENT APPLICATION NUMBER: US/09/596,002
; CURRENT FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: 60/140,121
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PERL Program
; SEQ ID NO 41
; LENGTH: 269223
; TYPE: DNA
; ORGANISM: Moraxella catarrhalis
; FEATURE:
; NAME/key: misc feature
; OTHER INFORMATION: Incyte template ID No. 6632636 41
; PUBLICATION INFORMATION:
US-09-596-002-41

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	Query Match	8.9%;	Score 136;	DB 4;	Length 269223;
	Best Local Similarity	100.0%;	Pred. No. 4.9e-61;		
	Matches 136;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	852	TAACGCAATAAGTAGACCGCTGGGGAGTAGCGCGCAAGGTTAAAACTCAAAATGAATTG	911		
Db	92136	TAACGCAATAAGTAGACCGCTGGGGAGTAGCGCGCAAGGTTAAAACTCAAAATGAATTG	92077		
Qy	912	ACGGGGGCCCGCACACAGCGGTGGAGCATGTGGTTTAATTCGATCGAACCGCGAAGAACCTT	971		
Db	92076	ACGGGGGCCCGCACACAGCGGTGGAGCATGTGGTTTAATTCGATCGAACCGCGAAGAACCTT	92017		
Qy	972	ACCTGGTCTTTGACATA	987		
Db	92016	ACCTGGTCTTTGACATA	92001		

```

RESULT 3
PCT-US91-01574-13
; Sequence 13, Application PC/TUS9101574
; GENERAL INFORMATION:
; APPLICANT: White Ph.D, Thomas J.
; APPLICANT: Dodge, Deborah E.
; TITLE OF INVENTION: Method for Diagnosis of Lyme Disease
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cetus Corporation
; STREET: 1400 Fifty-Third Street
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/01574
; FILING DATE: 19910307
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 489,676
; FILING DATE: 07-MAR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Kaster, Kevin R.
; REGISTRATION NUMBER: 32,704
; REFERENCE/DOCKET NUMBER: 2536.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 420-3444
; TELEFAX: (415) 658-5239
; TELEX: 4992659
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 881 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEetical: NO
; ANTI-SENSE: NO
; PCT-US91-01574-13

Query Match 7.9%; Score 121; DB 5; Length 881
Best Local Similarity 100.0%; Pred. NO. 4.5e-53;
Matches 121; Conservative 0; Mismatches 0; Indels

QY 866 GACCGCTGGGAGTACGCGCGCAAGTTTAAACTCAAATGAATTCGAC
DB 216 GACCGCTGGGAGTACGCGCGCAAGTTTAAACTCAAATGAATTCGAC
QY 926 AAGCGGTGGAGCATGTGGTTTAAATTCGATCGAACGCGAAGACCTTCAAC
DB 276 AAGCGGTGGAGCATGTGGTTTAAATTCGATCGAACGCGAAGACCTTCAAC
QY 986 T 986
DB 336 T 336

RESULT 4
US-07-923-871C-13
; Sequence 13, Application US/07923871C
; Patent No. 5912117
; GENERAL INFORMATION:
; APPLICANT: White Ph.D, Thomas J.
; APPLICANT: Dodge, Deborah E.
; TITLE OF INVENTION: Method for Diagnosis of Lyme Disease
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: NJ
; COUNTRY: USA
; ZIP: 07110-1199
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/923,871C
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 489,676

```

FILING DATE: 07-MAR-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Petry, Douglas A.  
REGISTRATION NUMBER: 35,321  
REFERENCE/DOCKET NUMBER: 8697  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (510) 814-2974  
TELEFAX: (510) 814-2977  
TELEX:  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 892 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-07-923-871C-13

Query Match 7.9%; Score 121; DB 2; Length 882;  
Best Local Similarity 100.0%; Pred. No. 4.4e-53;  
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 866 GACCGCTGGGAGTACGCGCGCAAGGTTAAACTCAAAATGAATGACGGGGCCCGCAC 925  
|  
DB 216 GACCGCTGGGAGTACGCGCGCAAGGTTAAACTCAAAATGAATGACGGGGCCCGCAC 275  
|  
QY 926 AAGCGGTGGAGCATGTGTTTAAATTCGATGCAACGCGAAGAACCTTACTTGCTTGACA 985  
|  
DB 276 AAGCGGTGGAGCATGTGTTTAAATTCGATGCAACGCGAAGAACCTTACTTGCTTGACA 335  
|  
QY 986 T 986  
|  
DB 336 T 336

RESULT 5  
US-09-726-774-14  
Sequence 14, Application US/09726774  
Patent No. 667153  
GENERAL INFORMATION:  
APPLICANT: Iversen, Patrick L.  
TITLE OF INVENTION: Antisense Antibacterial Method and  
FILE REFERENCE: 0450-0032.30  
CURRENT APPLICATION NUMBER: US/09/726,774  
CURRENT FILING DATE: 2000-11-29  
PRIOR FILING DATE: US 60/168,150  
NUMBER OF SEQ ID NOS: 139  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 14  
LENGTH: 1487  
TYPE: DNA  
ORGANISM: Shigella dysenterae  
US-09-726-774-14

Query Match 7.9%; Score 121; DB 4; Length 1487;  
Best Local Similarity 100.0%; Pred. No. 4.4e-53;  
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 866 GACCGCTGGGAGTACGCGCGCAAGGTTAAACTCAAAATGAATGACGGGGCCCGCAC 925  
|  
DB 857 GACCGCTGGGAGTACGCGCGCAAGGTTAAACTCAAAATGAATGACGGGGCCCGCAC 916  
|  
QY 926 AAGCGGTGGAGCATGTGTTTAAATTCGATGCAACGCGAAGAACCTTACTTGCTTGACA 985  
|  
DB 917 AAGCGGTGGAGCATGTGTTTAAATTCGATGCAACGCGAAGAACCTTACTTGCTTGACA 976  
|  
QY 986 T 986  
|  
DB 977 T 977

RESULT 6  
US-08-114-695A-1  
Sequence 1, Application US/08114695A  
Patent No. 5508193  
GENERAL INFORMATION:  
APPLICANT: Mandelbaum, Raphael T.  
TITLE OF INVENTION: DEGRADATION OF S-TRIAZINES IN SOIL AND  
TITLE OF INVENTION: WATER  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SCHWEGMAN, LUNDBERG & WOESSNER, P.A.  
STREET: 3500 IDS CENTER  
CITY: MINNEAPOLIS  
STATE: MN  
COUNTRY: USA  
ZIP: 55402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/114,695A  
FILING DATE: 31-AUG-1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: MUETING, ANN M.  
REGISTRATION NUMBER: 33,977  
REFERENCE/DOCKET NUMBER: 600,268US1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 612-339-0331  
TELEFAX: 612-339-3061  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1542 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: rRNA  
ORIGINAL SOURCE:  
ORGANISM: Escherichia coli  
US-08-114-695A-1

Query Match 7.9%; Score 121; DB 1; Length 1542;  
Best Local Similarity 80.2%; Pred. No. 4.4e-53;  
Matches 97; Conservative 24; Mismatches 0; Indels 0; Gaps 0;

QY 866 GACCGCTGGGAGTACGCGCGCAAGGTTAAACTCAAAATGAATGACGGGGCCCGCAC 925  
|  
DB 877 GACCGCTGGGAGTACGCGCGCAAGGTTAAACTCAAAATGAATGACGGGGCCCGCAC 936  
|  
QY 926 AAGCGGTGGAGCATGTGTTTAAATTCGATGCAACGCGAAGAACCTTACTTGCTTGACA 985  
|  
DB 917 AAGCGGTGGAGTACGCGCGCAAGGTTAAACTCAAAATGAATGACGGGGCCCGCAC 996  
|  
QY 986 T 986  
|  
DB 997 U 997

RESULT 7  
US-08-757-653-158  
Sequence 158, Application US/08757653  
Patent No. 5843669  
GENERAL INFORMATION:  
APPLICANT: Kaiser, Michael W.  
APPLICANT: Lyamichev, Victor I.  
APPLICANT: Lyamichev, Natasha  
TITLE OF INVENTION: Cleavage Of Nucleic Acid Using  
Thermostable FEN-1 Endonucleases

NUMBER OF SEQUENCES: 190  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Medlen & Carroll, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: California  
COUNTRY: United States Of America  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/757,653  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Ingolia, Diane E.  
REGISTRATION NUMBER: 40,027  
REFERENCE/DOCKET NUMBER: FORS-02565  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 158:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1542 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-757-653-158  
Query Match 7.9%; Score 121; DB 2; Length 1542;  
Best Local Similarity 100.0%; Pred. No. 4.4e-53;  
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 866 GACCGCTGGGAGTACGGCGCAAGGTTAAACTCAAAATGAATGACGGGGGGCCGCAC 925  
DB 877 GACCGCTGGGAGTACGGCGCAAGGTTAAACTCAAAATGAATGACGGGGGGCCGCAC 936  
QY 926 AAGCGGTGAGCATGTGTTTAAATTCGATGCAACGCGAAGACCTTACCTGGTCTTGACA 985  
DB 937 AAGCGGTGAGCATGTGTTTAAATTCGATGCAACGCGAAGACCTTACCTGGTCTTGACA 996  
QY 986 T 986  
DB 997 T 997  
RESULT 8  
US-09-465-355-2  
Sequence 2, Application US/09465355  
Patent No. 6316194  
GENERAL INFORMATION:  
APPLICANT: Karn, Jonathan  
APPLICANT: Knowles, David  
APPLICANT: Murchie, Alastair  
APPLICANT: Lentzen, Georg  
TITLE OF INVENTION: Methods and Kits for Discovery of RNA-Binding Antimicrobials  
FILE REFERENCE: 22620/1150 (Formerly 3950/85276)  
CURRENT APPLICATION NUMBER: US/09/465,355  
CURRENT FILING DATE: 1999-12-16  
PRIOR APPLICATION NUMBER: US 09/325,601  
PRIOR FILING DATE: 1999-06-03  
PRIOR APPLICATION NUMBER: GB 9812196.5  
PRIOR FILING DATE: 1998-06-05  
PRIOR APPLICATION NUMBER: GB 9904790.4  
PRIOR FILING DATE: 1999-03-02  
PRIOR APPLICATION NUMBER: US 60/122,439  
PRIOR FILING DATE: 1999-03-02  
PRIOR APPLICATION NUMBER: US 60/988,241  
PRIOR FILING DATE: 1998-06-05

NUMBER OF SEQ ID NOS: 37  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 2  
LENGTH: 1542  
TYPE: RNA  
ORGANISM: Escherichia coli  
US-09-465-355-2  
Query Match 7.9%; Score 121; DB 3; Length 1542;  
Best Local Similarity 80.2%; Pred. No. 4.4e-53;  
Matches 97; Conservative 24; Mismatches 0; Indels 0; Gaps 0;  
QY 866 GACCGCTGGGAGTACGGCGCAAGGTTAAACTCAAAATGAATGACGGGGGGCCGCAC 925  
DB 877 GACCGCTGGGAGTACGGCGCAAGGTTAAACTCAAAATGAATGACGGGGGGCCGCAC 936  
QY 926 AAGCGGTGAGCATGTGTTTAAATTCGATGCAACGCGAAGACCTTACCTGGTCTTGACA 985  
DB 937 AAGCGGTGAGCATGTGTTTAAATTCGATGCAACGCGAAGACCTTACCTGGTCTTGACA 996  
QY 986 T 986  
DB 997 U 997  
RESULT 9  
US-08-520-946-158  
Sequence 158, Application US/08520946  
Patent No. 6372424  
GENERAL INFORMATION:  
APPLICANT: BROW, MARY ANN D.  
APPLICANT: LYAMICHEV, VICTOR I.  
APPLICANT: OLIVE, DAVID M.  
TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF  
NUMBER OF SEQUENCES: 160  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL  
STREET: 220 MONTGOMERY STREET, SUITE 2200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: UNITED STATES OF AMERICA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/520,946  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: CARROLL, PETER G.  
REGISTRATION NUMBER: 32,837  
REFERENCE/DOCKET NUMBER: FORS-01756  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 158:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1542 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-520-946-158  
Query Match 7.9%; Score 121; DB 3; Length 1542;  
Best Local Similarity 100.0%; Pred. No. 4.4e-53;  
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 866 GACCGCTGGGAGTACGGCGCAAGGTTAAACTCAAAATGAATGACGGGGGGCCGCAC 925



Db 877 GACCGCTGGGAGTACGCGCGCAAGGTTAAACTCAAATGAATTCAGCGGGGCCGAC 936  
Qy 926 AAGCGGTGGAGCATGTGTTTAATTCGATGCAACCGGAAGAACCTTACCTGCTCTTGACA 985  
Db 937 AAGCGGTGGAGCATGTGTTTAATTCGATGCAACCGGAAGAACCTTACCTGCTCTTGACA 996  
Qy 986 T 986  
Db 997 T 997

RESULT 10  
US-09-655-378A-158  
; Sequence 158, Application US/09655378A  
; Patent No. 6673616  
; GENERAL INFORMATION:  
; APPLICANT: BROW, MARY ANN D.  
; LYAMICHEV, VICTOR I.  
; OLIVE, DAVID M.  
; TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF  
; PATHOGENS  
; NUMBER OF SEQUENCES: 165  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MEDLEN & CARROLL  
; STREET: 220 MONTGOMERY STREET, SUITE 2200  
; CITY: SAN FRANCISCO  
; STATE: CALIFORNIA  
; COUNTRY: UNITED STATES OF AMERICA  
; ZIP: 94104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/655,378A  
; FILING DATE: 05-Sep-2000  
; CLASSIFICATION: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CARROLL, PETER G.  
; REGISTRATION NUMBER: 32,837  
; REFERENCE/DOCKET NUMBER: FORS-01756  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 705-8410  
; TELEFAX: (415) 397-8338  
; INFORMATION FOR SEQ ID NO: 158:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1542 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (Genomic)  
; SEQUENCE DESCRIPTION: SEQ ID NO: 158:  
US-09-655-378A-158

Query Match 7.9%; Score 121; DB 4; Length 1542;  
Best Local Similarity 100.0%; Pred. No. 4.4e-53;  
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 866 GACCGCTGGGAGTACGCGCGCAAGGTTAAACTCAAATGAATTCAGCGGGGCCGAC 925  
Db 877 GACCGCTGGGAGTACGCGCGCAAGGTTAAACTCAAATGAATTCAGCGGGGCCGAC 936  
Qy 926 AAGCGGTGGAGCATGTGTTTAATTCGATGCAACCGGAAGAACCTTACCTGCTCTTGACA 985  
Db 937 AAGCGGTGGAGCATGTGTTTAATTCGATGCAACCGGAAGAACCTTACCTGCTCTTGACA 996  
Qy 986 T 986  
Db 997 T 997

RESULT 11  
US-09-548-998E-33  
; Sequence 33, Application US/09548998E  
; Patent No. 6797817  
; GENERAL INFORMATION:  
; APPLICANT: E.I. DUPONT DE NEMOURS & COMPANY, INC.  
; APPLICANT: EBERSOLE, RICHARD C.  
; APPLICANT: HENDRICKSON, EDWIN  
; TITLE OF INVENTION: NUCLEIC ACID FRAGMENTS FOR THE IDENTIFICATION OF DECHLORINATING B  
; FILE REFERENCE: BC1002 US NA  
; CURRENT APPLICATION NUMBER: US/09/548,998E  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/129,511  
; PRIOR FILING DATE: 1999-04-15  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 33  
; LENGTH: 1542  
; TYPE: DNA  
; ORGANISM: Escherichia coli  
US-09-548-998E-33

Query Match 7.9%; Score 121; DB 4; Length 1542;  
Best Local Similarity 100.0%; Pred. No. 4.4e-53;  
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 866 GACCGCTGGGAGTACGCGCGCAAGGTTAAACTCAAATGAATTCAGCGGGGCCGAC 925  
Db 877 GACCGCTGGGAGTACGCGCGCAAGGTTAAACTCAAATGAATTCAGCGGGGCCGAC 936  
Qy 926 AAGCGGTGGAGCATGTGTTTAATTCGATGCAACCGGAAGAACCTTACCTGCTCTTGACA 985  
Db 937 AAGCGGTGGAGCATGTGTTTAATTCGATGCAACCGGAAGAACCTTACCTGCTCTTGACA 996  
Qy 986 T 986  
Db 997 T 997

RESULT 12  
US-09-492-709A-89  
; Sequence 89, Application US/09492709A  
; Patent No. 6720139  
; GENERAL INFORMATION:  
; APPLICANT: Zyskind, Judith  
; APPLICANT: Ohlsen, Kari L.  
; APPLICANT: Trawick, John  
; APPLICANT: Forsyth, R. Allyn  
; APPLICANT: Froelich, Jamie M.  
; APPLICANT: Carr, Grant J.  
; APPLICANT: Yamamoto, Robert T.  
; APPLICANT: Xu, H. Howard  
; TITLE OF INVENTION: GENES IDENTIFIED AS REQUIRED FOR PROLIFERATION IN  
; FILE REFERENCE: ELITRA.001A  
; CURRENT APPLICATION NUMBER: US/09/492,709A  
; CURRENT FILING DATE: 2000-01-27  
; NUMBER OF SEQ ID NOS: 485  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 89  
; LENGTH: 1549  
; TYPE: DNA  
; ORGANISM: E. Coli  
US-09-492-709A-89

Query Match 7.9%; Score 121; DB 4; Length 1549;  
Best Local Similarity 100.0%; Pred. No. 4.4e-53;  
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 866 GACCGCTGGGAGTACGCGCGCAAGGTTAAACTCAAATGAATTCAGCGGGGCCGAC 925  
Db 878 GACCGCTGGGAGTACGCGCGCAAGGTTAAACTCAAATGAATTCAGCGGGGCCGAC 937



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: April 12, 2005, 12:56:39 ; Search time 940 Seconds  
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Scoring table: OLIGO\_NUC  
Gapop 60.0, Gapext 60.0

Searched: 5615251 seqs, 3030001701 residues  
Word size : 0  
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Minimum DB seq length: 0  
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Post-processing: Listing first 45 summaries

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3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq.\*  
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7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq.\*  
8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq.\*  
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10: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq.\*  
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17: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq.\*  
18: /cgn2\_6/ptodata/1/pubpna/US10F\_PUBCOMB.seq.\*  
19: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq.\*  
20: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq.\*  
21: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq.\*  
22: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	121	7.9	549	10	US-09-991-936-1717
3	121	7.9	1487	9	US-09-726-774-14
4	121	7.9	1487	18	US-10-719-633-14
5	121	7.9	1505	9	US-09-027-439-6
6	121	7.9	1506	9	US-09-027-439-3
7	121	7.9	1534	16	US-10-029-397A-35
8	121	7.9	1541	9	US-09-027-439-7
9	121	7.9	1542	10	US-09-940-925A-158
10	121	7.9	1542	10	US-09-941-193A-158
11	121	7.9	1542	14	US-10-061-071-33

12	121	7.9	1549	9	US-09-912-020-89	Sequence 89, Appl
13	121	7.9	1549	9	US-09-912-020-242	Sequence 242, App
14	121	7.9	1549	9	US-09-912-020-402	Sequence 402, App
15	121	7.9	1549	18	US-10-771-241-89	Sequence 89, Appl
16	121	7.9	1549	18	US-10-771-241-242	Sequence 242, App
17	121	7.9	1549	18	US-10-771-241-402	Sequence 402, App
c 18	121	7.9	10903	18	US-10-612-224-1	Sequence 1, Appli
c 19	121	7.9	11918	18	US-10-612-224-2	Sequence 2, Appli
20	121	7.9	13278	18	US-10-612-224-3	Sequence 3, Appli
21	116	7.6	1494	13	US-10-007-725-5	Sequence 5, Appli
22	114	7.5	1541	9	US-09-726-774-2	Sequence 2, Appli
23	114	7.5	1541	18	US-10-719-633-2	Sequence 2, Appli
24	112	7.3	1324	18	US-10-808-807-16	Sequence 16, Appl
25	112	7.3	1331	18	US-10-804-677-16	Sequence 16, Appl
26	110	7.2	1327	18	US-10-808-979-16	Sequence 16, Appl
27	110	7.2	1351	19	US-10-810-733-18	Sequence 18, Appl
28	110	7.2	1455	18	US-10-761-509-1	Sequence 1, Appli
29	110	7.2	1485	16	US-10-029-397A-36	Sequence 36, Appl
30	110	7.2	1830121	17	US-10-329-670-1	Sequence 1, Appli
c 31	110	7.2	1830121	17	US-10-329-670-1	Sequence 1, Appli
32	110	7.2	1830121	18	US-10-158-865-1	Sequence 1, Appli
c 33	110	7.2	1830121	18	US-10-158-865-1	Sequence 1, Appli
34	109	7.1	1506	16	US-10-378-942-1	Sequence 1, Appli
35	108	7.1	1486	9	US-09-737-297-1	Sequence 1, Appli
36	101	6.6	1542	18	US-10-361-002-6	Sequence 6, Appli
37	101	6.6	1542	18	US-10-361-004-6	Sequence 6, Appli
38	99	6.5	1453	9	US-09-027-439-5	Sequence 5, Appli
39	95	6.2	1481	9	US-09-737-297-4	Sequence 4, Appli
40	94	6.2	1131	18	US-10-704-751-1	Sequence 1, Appli
41	88	5.8	1070	9	US-09-737-297-2	Sequence 2, Appli
42	88	5.8	1140	9	US-09-737-297-5	Sequence 5, Appli
43	88	5.8	1420	19	US-10-875-006-1	Sequence 1, Appli
44	88	5.8	1424	14	US-10-007-527A-12	Sequence 12, Appl
45	88	5.8	1424	14	US-10-007-452-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1

US-10-672-787-41/c  
; Sequence 41, Application US/10672787  
; Publication No. US20040067554A1  
; GENERAL INFORMATION:  
; APPLICANT: LAGACE, Robert, E.  
; APPLICANT: PATTERSON, Chandra  
; APPLICANT: BERG, Kim, L.  
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF MORAXELLA CATARRHALIS GENOME  
; FILE REFERENCE: ELITRA.025C1  
; CURRENT APPLICATION NUMBER: US/10/672,787  
; CURRENT FILING DATE: 2003-09-26  
; PRIOR APPLICATION NUMBER: 09/596,002  
; PRIOR FILING DATE: 2000-06-16  
; NUMBER OF SEQ ID NOS: 41  
; SOFTWARE: PERL Program  
; SEQ ID NO 41  
; LENGTH: 269223  
; TYPE: DNA  
; ORGANISM: Moraxella catarrhalis  
US-10-672-787-41

Query Match	8.9%	Score 136;	DB 17;	Length 269223;
Best Local Similarity	100.0%;	Pred. No. 9e-62;		
Matches 136;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	852	TAAAGCAATAGTAGACCGCTGGGGAGTAGCGCGCAAGGTTAAACTCAATGAATTG	911	
Db	92136	TAAAGCAATAGTAGACCGCTGGGGAGTAGCGCGCAAGGTTAAACTCAATGAATTG	92077	
Qy	912	ACGGGGCCCGCACCAAGCGGTGGAGCATGTGTTTAAATTCGATCAACGCCGAAGACCTT	971	
Db	92076	ACGGGGCCCGCACCAAGCGGTGGAGCATGTGTTTAAATTCGATCAACGCCGAAGACCTT	92017	

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QY 972 ACCTGGTCTTGACATA 987
Db 92016 ACCTGGTCTTGACATA 92001

RESULT 2
US-09-991-936-1717
; Sequence 1717, Application US/09991936
; Publication No. US20030073827A1
; GENERAL INFORMATION:
; APPLICANT: Brandt, Kevin S.
; APPLICANT: Gaines, Patrick J.
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Wisniewski, Nancy
; TITLE OF INVENTION: FLEA HEAD, NERVE CORD, HINDGUT AND MALPIGHIAN TUBULE
; FILE OF INVENTION: NUCLEIC ACID MOLECULES, PROTEINS AND USES THEREOF
; FILE REFERENCE: FC-6-C1
; CURRENT APPLICATION NUMBER: US/09/991,936
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US/09/543,668
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 60/128,704
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 1959
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1717
; LENGTH: 549
; TYPE: DNA
; ORGANISM: Ctenocephalides felis
US-09-991-936-1717

Query Match 7.9%; Score 121; DB 10; Length 549;
Best Local Similarity 100.0%; Pred. No. 1.4e-53;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 866 GACCGCTGGGAGTACGGCGCAAGGTTAAACTCAAATGAATTCACGGGGGCGCCGAC 925
Db 163 GACCGCTGGGAGTACGGCGCAAGGTTAAACTCAAATGAATTCACGGGGGCGCCGAC 222

QY 926 AAGCGGTGGAGCATGTGGTTTAATTCGATCGAACGCGAAGAACCTTACCTGGTCTTGACA 985
Db 223 AAGCGGTGGAGCATGTGGTTTAATTCGATCGAACGCGAAGAACCTTACCTGGTCTTGACA 282

QY 986 T 986
Db 283 T 283

RESULT 3
US-09-726-774-14
; Sequence 14, Application US/09726774
; Patent No. US20020082226A1
; GENERAL INFORMATION:
; APPLICANT: Iversen, Patrick L.
; TITLE OF INVENTION: Antisense Antibacterial Method and
; FILE OF INVENTION: Composition
; FILE REFERENCE: 0450-0032.30
; CURRENT APPLICATION NUMBER: US/09/726,774
; CURRENT FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: US 60/168,150
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 139
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 1487
; TYPE: DNA
; ORGANISM: Shigella dysenteriae
US-09-726-774-14

Query Match 7.9%; Score 121; DB 9; Length 1487;
Best Local Similarity 100.0%; Pred. No. 1.3e-53;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 926 AAGCGGTGGAGCATGTGGTTTAATTCGATCGAACGCGAAGAACCTTACCTGGTCTTGACA 985
Db 223 AAGCGGTGGAGCATGTGGTTTAATTCGATCGAACGCGAAGAACCTTACCTGGTCTTGACA 282

QY 986 T 986
Db 283 T 283

RESULT 4
US-10-719-633-14
; Sequence 14, Application US/10719633
; Publication No. US20040137485A1
; GENERAL INFORMATION:
; APPLICANT: Iversen, Patrick L.
; TITLE OF INVENTION: Antisense Antibacterial Method and
; FILE OF INVENTION: Composition
; FILE REFERENCE: 0450-0032.30
; CURRENT APPLICATION NUMBER: US/10/719,633
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: US/09/726,774
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: US 60/168,150
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 139
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 1487
; TYPE: DNA
; ORGANISM: Shigella dysenterae
US-10-719-633-14

Query Match 7.9%; Score 121; DB 18; Length 1487;
Best Local Similarity 100.0%; Pred. No. 1.3e-53;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 926 AAGCGGTGGAGCATGTGGTTTAATTCGATCGAACGCGAAGAACCTTACCTGGTCTTGACA 985
Db 917 AAGCGGTGGAGCATGTGGTTTAATTCGATCGAACGCGAAGAACCTTACCTGGTCTTGACA 976

QY 986 T 986
Db 977 T 977

RESULT 5
US-09-027-439-6
; Sequence 6, Application US/09027439A
; Patent No. US20020006611A1
; GENERAL INFORMATION:
; APPLICANT: Portugal, Frank H.
; APPLICANT: Colwell, Rita R.
; APPLICANT: Hug, Anwarul
; APPLICANT: Chowdhury, Afzal
; TITLE OF INVENTION: Compositions and Methods for Differentiating Among
; FILE OF INVENTION: Shigella Species and Shigella from E. coli Species
; FILE REFERENCE: 044198/0000
; CURRENT APPLICATION NUMBER: US/09/027,439A
; CURRENT FILING DATE: 1998-02-20
; EARLIER APPLICATION NUMBER: 60/038,117
; EARLIER FILING DATE: 1997-02-20
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1505

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Publication No. US20030054338A1  
GENERAL INFORMATION:  
APPLICANT: BROW, MARY ANN D.  
LYAMICHEV, VICTOR I.  
OLIVE, DAVID M.  
TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF  
PATHOGENS  
NUMBER OF SEQUENCES: 165  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL  
STREET: 220 MONTGOMERY STREET, SUITE 2200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: UNITED STATES OF AMERICA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/940,925A  
FILING DATE: 10-Jun-2002  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: CARROLL, PETER G.  
REGISTRATION NUMBER: 32,837  
REFERENCE/DOCKET NUMBER: FORS-01756  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 158:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1542 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
SEQUENCE DESCRIPTION: SEQ ID NO: 158:  
US-09-940-925A-158  
Query Match 7.9%; Score 121; DB 10; Length 1542;  
Best Local Similarity 100.0%; Pred. No. 1.3e-53;  
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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877 GACCGCTGGGAGTAGCGCGCAAGGTTAAACTCAAACTCAAAATGAATTGACGGGGCCCCGCAC 936  
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937 AAGCGGTGGAGCATGTGTTTAATTCGATGCAACGCGAAGAACCTTACCTGGTCTTGACA 996  
Qy 986 T 986  
Db 997 T 997  
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US-09-941-193A-158  
Sequence 158, Application US/09941193A  
Publication No. US20030108873A1  
GENERAL INFORMATION:  
APPLICANT: BROW, MARY ANN D.  
LYAMICHEV, VICTOR I.  
OLIVE, DAVID M.  
TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF  
PATHOGENS  
NUMBER OF SEQUENCES: 165  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL  
STREET: 220 MONTGOMERY STREET, SUITE 2200  
CITY: SAN FRANCISCO

STATE: CALIFORNIA  
COUNTRY: UNITED STATES OF AMERICA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/941,193A  
FILING DATE: 28-Aug-2001  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: CARROLL, PETER G.  
REGISTRATION NUMBER: 32,837  
REFERENCE/DOCKET NUMBER: FORS-01756  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 158:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1542 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
SEQUENCE DESCRIPTION: SEQ ID NO: 158:  
US-09-941-193A-158  
Query Match 7.9%; Score 121; DB 10; Length 1542;  
Best Local Similarity 100.0%; Pred. No. 1.3e-53;  
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 866 GACCGCTGGGAGTAGCGCGCAAGGTTAAACTCAAACTCAAAATGAATTGACGGGGCCCCGCAC 925  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
877 GACCGCTGGGAGTAGCGCGCAAGGTTAAACTCAAACTCAAAATGAATTGACGGGGCCCCGCAC 936  
Qy 926 AAGCGGTGGAGCATGTGTTTAATTCGATGCAACGCGAAGAACCTTACCTGGTCTTGACA 985  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
937 AAGCGGTGGAGCATGTGTTTAATTCGATGCAACGCGAAGAACCTTACCTGGTCTTGACA 996  
Qy 986 T 986  
Db 997 T 997  
RESULT 11  
US-10-061-071-33  
Sequence 33, Application US/10061071  
Publication No. US20030077601A1  
GENERAL INFORMATION:  
APPLICANT: E.I. DUPONT DE NEMOURS & COMPANY  
APPLICANT: HENDRICKSON, EDWIN  
TITLE OF INVENTION: NUCLEIC ACID FRAGMENTS FOR THE IDENTIFICATION OF DECHLORINATING  
BACTERIA  
FILE REFERENCE: BC1002 US CIP  
CURRENT APPLICATION NUMBER: US/10/061,071  
CURRENT FILING DATE: 2002-01-29  
PRIOR APPLICATION NUMBER: US 60/129,511  
PRIOR FILING DATE: 1999-04-15  
PRIOR APPLICATION NUMBER: 60/129,511  
PRIOR FILING DATE: 1999-04-15  
NUMBER OF SEQ ID NOS: 103  
SOFTWARE: Microsoft Office 97  
SEQ ID NO 33  
LENGTH: 1542  
TYPE: DNA  
ORGANISM: Escherichia coli  
US-10-061-071-33  
Query Match 7.9%; Score 121; DB 14; Length 1542;  
Best Local Similarity 100.0%; Pred. No. 1.3e-53;  
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 866 GACCGCTGGGAGTACGGCCGCAAGGTTAAACTCAAACTCAAAATGAATGACGGGGCCCGCAC 925  
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Db 877 GACCGCTGGGAGTACGGCCGCAAGGTTAAACTCAAACTCAAAATGAATGACGGGGCCCGCAC 936  
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Qy 926 AAGCGTGGAGCATGTGTTTAAATTCGATGCAACCGGAAGAACCTTACCTGGTCTTGACA 985  
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Db 937 AAGCGTGGAGCATGTGTTTAAATTCGATGCAACCGGAAGAACCTTACCTGGTCTTGACA 996  
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Qy 986 T 986  
|  
Db 997 T 997

RESULT 12  
US-09-912-020-89  
; Sequence 89, Application US/09912020  
; Patent No. US20020045592A1  
; GENERAL INFORMATION:  
; APPLICANT: Zyskind, Judith  
; APPLICANT: Ohlsen, Kari L.  
; APPLICANT: Trawick, John  
; APPLICANT: Forsyth, R. Allyn  
; APPLICANT: Froelich, Jamie M.  
; APPLICANT: Carr, Grant J.  
; APPLICANT: Yamamoto, Robert T.  
; APPLICANT: Xu, H. Howard  
; TITLE OF INVENTION: GENES IDENTIFIED AS REQUIRED FOR PROLIFERATION IN  
; FILE REFERENCE: ELITRA.001DV1  
; CURRENT APPLICATION NUMBER: US/09/912,020  
; CURRENT FILING DATE: 2001-07-23  
; PRIOR APPLICATION NUMBER: 09/492,709  
; PRIOR FILING DATE: 2000-01-27  
; PRIOR APPLICATION NUMBER: 60/117,405  
; PRIOR FILING DATE: 1999-01-27  
; NUMBER OF SEQ ID NOS: 485  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 89  
; LENGTH: 1549  
; TYPE: DNA  
; ORGANISM: E. Coli  
US-09-912-020-89

Query Match 7.9%; Score 121; DB 9; Length 1549;  
Best Local Similarity 100.0%; Pred. No. 1.3e-53;  
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 866 GACCGCTGGGAGTACGGCCGCAAGGTTAAACTCAAACTCAAAATGAATGACGGGGCCCGCAC 925  
|  
Db 878 GACCGCTGGGAGTACGGCCGCAAGGTTAAACTCAAACTCAAAATGAATGACGGGGCCCGCAC 937  
|  
Qy 926 AAGCGTGGAGCATGTGTTTAAATTCGATGCAACCGGAAGAACCTTACCTGGTCTTGACA 985  
|  
Db 938 AAGCGTGGAGCATGTGTTTAAATTCGATGCAACCGGAAGAACCTTACCTGGTCTTGACA 997  
|  
Qy 986 T 986  
|  
Db 998 T 998

RESULT 13  
US-09-912-020-242  
; Sequence 242, Application US/09912020  
; Patent No. US20020045592A1  
; GENERAL INFORMATION:  
; APPLICANT: Zyskind, Judith  
; APPLICANT: Ohlsen, Kari L.  
; APPLICANT: Trawick, John  
; APPLICANT: Forsyth, R. Allyn  
; APPLICANT: Froelich, Jamie M.  
; APPLICANT: Carr, Grant J.  
; APPLICANT: Yamamoto, Robert T.

; APPLICANT: Xu, H. Howard  
; TITLE OF INVENTION: GENES IDENTIFIED AS REQUIRED FOR PROLIFERATION IN  
; FILE REFERENCE: ELITRA.001DV1  
; CURRENT APPLICATION NUMBER: US/09/912,020  
; CURRENT FILING DATE: 2001-07-23  
; PRIOR APPLICATION NUMBER: 09/492,709  
; PRIOR FILING DATE: 2000-01-27  
; PRIOR APPLICATION NUMBER: 60/117,405  
; PRIOR FILING DATE: 1999-01-27  
; NUMBER OF SEQ ID NOS: 485  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 242  
; LENGTH: 1549  
; TYPE: DNA  
; ORGANISM: E. Coli  
US-09-912-020-242

Query Match 7.9%; Score 121; DB 9; Length 1549;  
Best Local Similarity 100.0%; Pred. No. 1.3e-53;  
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 866 GACCGCTGGGAGTACGGCCGCAAGGTTAAACTCAAACTCAAAATGAATGACGGGGCCCGCAC 925  
|  
Db 878 GACCGCTGGGAGTACGGCCGCAAGGTTAAACTCAAACTCAAAATGAATGACGGGGCCCGCAC 937  
|  
Qy 926 AAGCGTGGAGCATGTGTTTAAATTCGATGCAACCGGAAGAACCTTACCTGGTCTTGACA 985  
|  
Db 938 AAGCGTGGAGCATGTGTTTAAATTCGATGCAACCGGAAGAACCTTACCTGGTCTTGACA 997  
|  
Qy 986 T 986  
|  
Db 998 T 998

RESULT 14  
US-09-912-020-402  
; Sequence 402, Application US/09912020  
; Patent No. US20020045592A1  
; GENERAL INFORMATION:  
; APPLICANT: Zyskind, Judith  
; APPLICANT: Ohlsen, Kari L.  
; APPLICANT: Trawick, John  
; APPLICANT: Forsyth, R. Allyn  
; APPLICANT: Froelich, Jamie M.  
; APPLICANT: Carr, Grant J.  
; APPLICANT: Yamamoto, Robert T.  
; APPLICANT: Xu, H. Howard  
; TITLE OF INVENTION: GENES IDENTIFIED AS REQUIRED FOR PROLIFERATION IN  
; FILE REFERENCE: ELITRA.001DV1  
; CURRENT APPLICATION NUMBER: US/09/912,020  
; CURRENT FILING DATE: 2001-07-23  
; PRIOR APPLICATION NUMBER: 09/492,709  
; PRIOR FILING DATE: 2000-01-27  
; PRIOR APPLICATION NUMBER: 60/117,405  
; PRIOR FILING DATE: 1999-01-27  
; NUMBER OF SEQ ID NOS: 485  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 402  
; LENGTH: 1549  
; TYPE: RNA  
; ORGANISM: E. Coli  
US-09-912-020-402

Query Match 7.9%; Score 121; DB 9; Length 1549;  
Best Local Similarity 80.2%; Pred. No. 1.3e-53;  
Matches 97; Conservative 24; Mismatches 0; Indels 0; Gaps 0;  
Qy 866 GACCGCTGGGAGTACGGCCGCAAGGTTAAACTCAAACTCAAAATGAATGACGGGGCCCGCAC 925  
|  
Db 878 GACCGCTGGGAGTACGGCCGCAAGGTTAAACTCAAACTCAAAATGAATGACGGGGCCCGCAC 937  
|





GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: April 12, 2005, 10:39:14 ; Search time 5290 Seconds  
(without alignments)  
10980.354 Million cell updates/sec

Title: US-09-979-558A-1  
Perfect score: 1526  
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Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 34239544 seqs, 19032134700 residues

Word size : 0

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : EST:  
1: gb\_est1:  
2: gb\_est2:  
3: gb\_hic:  
4: gb\_est3:  
5: gb\_est4:  
6: gb\_est5:  
7: gb\_est6:  
8: gb\_gse1:  
9: gb\_gse2:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	121	7.9	247	CB393967	OSTR129G4
2	121	7.9	394	BH819649	BACPP13-M
3	121	7.9	437	BH835798	BACPP9-A0
4	121	7.9	465	BG357866	OV2_31-C0
5	121	7.9	473	BH831257	BACPP33-C
6	121	7.9	522	BH826849	BACPP24-C
7	121	7.9	524	BH822044	BACPP17-A
8	121	7.9	542	CF339295	RCL1--04-
9	121	7.9	592	AG019018	Homo sapi
10	121	7.9	609	BQ152671	NF022A12I
11	121	7.9	639	BH818000	BACPP10-K
12	121	7.9	646	BH822078	BACPP17-E
13	121	7.9	646	BH833826	BACPP5-P0
14	121	7.9	658	CF339842	RCL1--06-
15	121	7.9	661	BH820342	BACPP14-O
16	121	7.9	745	CF566443	1115107G1
17	121	7.9	770	CF557211	1115025D0
18	121	7.9	861	CL689507	PR10151b
19	121	7.9	1238	CG753740	P048-4-G0
20	103	6.7	516	AG613313	Escherich
21	99	6.5	714	BE202334	SNOWMFCAR
22	94	6.2	383	BE427965	MTD001-1.
23	88	5.8	502	AU312474	AU312474
24	88	5.8	676	BE187622	EST336183

25	88	5.8	735	6	CD423027	CD423027 SA1_29_G0
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28	88	5.8	1205	8	BZ566538	pacB2-184
29	88	5.8	1507	8	BZ576476	msh2_4950
30	86	5.6	184	2	AW834377	MR2-TT001
31	86	5.6	503	6	CD423957	SA1_2_B04
32	86	5.6	516	4	BM335455	MEST162-A
33	86	5.6	521	4	BM332487	MEST169-P
34	86	5.6	527	4	BM348070	MEST286-B
35	86	5.6	559	2	BF845685	780B5 CDN
36	86	5.6	569	1	A1779239	EST260118
37	86	5.6	604	2	BE204135	EST396811
38	86	5.6	660	2	AW600903	3B5 cDNA
39	86	5.6	851	7	CK290947	EST753661
40	86	5.6	884	7	CK280528	EST743250
41	86	5.6	889	7	CK280527	EST743249
42	86	5.6	941	7	CK296497	EST759211
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ALIGNMENTS

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LOCUS OSTR129G4\_1 AD-wrmcDNA Caenorhabditis elegans cDNA, linear EST 15-MAY-2003  
DEFINITION CB393967  
ACCESSION CB393967  
VERSION CB393967.1 GI:30735678  
KEYWORDS EST.  
SOURCE Caenorhabditis elegans  
ORGANISM Caenorhabditis elegans  
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;  
Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.  
REFERENCE 1 (bases 1 to 247)  
AUTHORS Reoul,J., Vaglio,P., Rual,J.F., Lanesch,P., Martinez,M.,  
Armstrong,C.M., Li,S., Jacotot,L., Bertin,N., Janky,R., Moore,T.,  
Hudson,J.R., Hartley,J.L., Brasch,M.A., Vandenhaute,J., Boulton,S.,  
Endress,G.A., Jenna,S., Chevet,E., Papasotiropoulos,V.,  
Tolias,P.P., Ptacek,J., Snyder,M., Huang,R., Chance,M.R., Lee,H.,  
Doucette-Stamm,L., Hill,D.E. and Vidal,M.  
C. elegans ORFeome version 1.1: experimental verification of the  
genome annotation and resource for proteome-scale protein  
expression  
Nat. Genet. (2003) In press  
Contact: Vidal M  
Marc Vidal Laboratory  
Dana Farber Cancer Institute  
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA  
Tel: 617 632 5180  
Fax: 617 632 5739  
Email: Marc.Vidal@dfci.harvard.edu  
Sequence tag of Gateway entry clones. The primers used were  
designed on the predicted protein encoding ORF. C. elegans ORFeome  
cloning project : Contact david\_hill@dfci.harvard.edu or  
marc\_vidal@dfci.harvard.edu  
POLYA=No.

JOURNAL COMMENT

Location/Qualifiers  
1. .247  
/organism="Caenorhabditis elegans"  
/mol\_type="mRNA"  
/db\_xref="taxon:6239"  
/sex="Hermaphrodite and male"  
/tissue\_type="whole animal"  
/dev\_stage="mixed stage"  
/clone\_lib="AD-wrmcDNA"  
/note="The AD-wrmcDNA library was generated with poly(A)+  
RNA isolated from both hermaphrodite and male N2 worms of  
all larval stages, embryos, adults and dauers and the

FEATURES

Source  
1. .247  
/organism="Caenorhabditis elegans"  
/mol\_type="mRNA"  
/db\_xref="taxon:6239"  
/sex="Hermaphrodite and male"  
/tissue\_type="whole animal"  
/dev\_stage="mixed stage"  
/clone\_lib="AD-wrmcDNA"  
/note="The AD-wrmcDNA library was generated with poly(A)+  
RNA isolated from both hermaphrodite and male N2 worms of  
all larval stages, embryos, adults and dauers and the

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subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into pPC86"

ORIGIN
Query Match          7.9%; Score 121; DB 6; Length 247;
Best Local Similarity 100.0%; Pred. No. 2.3e-56;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 866 GACCGCTGGGAGTACGGCGCAAGGTTAAATTCGATGCAACGCGAAGAACCTTACCTGGTCTTGACA 925
Db 64 GACCGCTGGGAGTACGGCGCAAGGTTAAATTCGATGCAACGCGAAGAACCTTACCTGGTCTTGACA 123
Qy 926 AAGCGGTGGAGCATGTGGTTTAAATTCGATGCAACGCGAAGAACCTTACCTGGTCTTGACA 985
Db 124 AAGCGGTGGAGCATGTGGTTTAAATTCGATGCAACGCGAAGAACCTTACCTGGTCTTGACA 183
Qy 986 T 986
Db 184 T 184

RESULT 2
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LOCUS
DEFINITION
BACPP13-M12.y Pristionchus pacificus BAC ends Pristionchus
pacificus genomic, genomic survey sequence.
ACCESSION
BH819649
VERSION
BH819649.1 GI:20993980
SOURCE
Pristionchus pacificus
ORGANISM
Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
REFERENCE
1 (bases 1 to 394)
Raddatz,G., Witte,H., Keller,H., Lanz,W., Brand,A., Nandakumar,R.,
Jesse,T., Mollare,J., de Both,M., Schuster,S.C. and Sommer,R.J.
A BAC-based genetic linkage map of the nematode Pristionchus
pacificus
JOURNAL
Unpublished (2002)
COMMENT
Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
Class: BAC ends.
Location/Qualifiers
1..394
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="var. California"
/db_xref="taxon:54126"
/clone_lib="Pristionchus pacificus BAC ends"

ORIGIN
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Best Local Similarity 100.0%; Pred. No. 2.3e-56;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 866 GACCGCTGGGAGTACGGCGCAAGGTTAAATTCGATGCAACGCGAAGAACCTTACCTGGTCTTGACA 925
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Qy 926 AAGCGGTGGAGCATGTGGTTTAAATTCGATGCAACGCGAAGAACCTTACCTGGTCTTGACA 985
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Qy 986 T 986
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source
1..394
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="var. California"
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ORIGIN
Query Match          7.9%; Score 121; DB 8; Length 394;
Best Local Similarity 100.0%; Pred. No. 2.3e-56;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 866 GACCGCTGGGAGTACGGCGCAAGGTTAAATTCGATGCAACGCGAAGAACCTTACCTGGTCTTGACA 925
Db 223 GACCGCTGGGAGTACGGCGCAAGGTTAAATTCGATGCAACGCGAAGAACCTTACCTGGTCTTGACA 282
Qy 926 AAGCGGTGGAGCATGTGGTTTAAATTCGATGCAACGCGAAGAACCTTACCTGGTCTTGACA 985
Db 283 AAGCGGTGGAGCATGTGGTTTAAATTCGATGCAACGCGAAGAACCTTACCTGGTCTTGACA 342
Qy 986 T 986
Db 343 T 343

RESULT 3
BH835798
LOCUS
DEFINITION
BACPP9-A07.2 Pristionchus pacificus BAC ends Pristionchus pacificus
genomic, genomic survey sequence.
ACCESSION
BH835798
VERSION
BH835798.1 GI:21038085
SOURCE
Pristionchus pacificus
ORGANISM
Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
REFERENCE
1 (bases 1 to 437)
Srinivasan,J., Sinz,W., Lanz,C., Brand,A., Nandakumar,R.,
Raddatz,G., Witte,H., Keller,H., Kipping,I., Pires da Silva,A.,
Jesse,T., Mollare,J., de Both,M., Schuster,S.C. and Sommer,R.J.
A BAC-based genetic linkage map of the nematode Pristionchus
pacificus
JOURNAL
Unpublished (2002)
COMMENT
Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
Class: BAC ends.
Location/Qualifiers
1..437
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="var. California"
/db_xref="taxon:54126"
/clone_lib="Pristionchus pacificus BAC ends"

ORIGIN
Query Match          7.9%; Score 121; DB 8; Length 437;
Best Local Similarity 100.0%; Pred. No. 2.3e-56;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 866 GACCGCTGGGAGTACGGCGCAAGGTTAAATTCGATGCAACGCGAAGAACCTTACCTGGTCTTGACA 925
Db 220 GACCGCTGGGAGTACGGCGCAAGGTTAAATTCGATGCAACGCGAAGAACCTTACCTGGTCTTGACA 279
Qy 926 AAGCGGTGGAGCATGTGGTTTAAATTCGATGCAACGCGAAGAACCTTACCTGGTCTTGACA 985
Db 280 AAGCGGTGGAGCATGTGGTTTAAATTCGATGCAACGCGAAGAACCTTACCTGGTCTTGACA 339
Qy 986 T 986
Db 340 T 340

RESULT 4
BG357866
LOCUS
DEFINITION
OV2_31_C04.bl_A002 Ovary 2 (OV2) Sorghum bicolor cDNA, mRNA
sequence.
ACCESSION
BG357866
VERSION
BG357866.1 GI:13239852
SOURCE
Sorghum bicolor (sorghum)
ORGANISM
Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD
clade; Panicoideae; Andropogoneae; Sorghum.
REFERENCE
1 (bases 1 to 465)
Cordonnier-Pratt,M.-M., Gingle,A., Marsala,C., Sudman,M. and
Pratt,L.H.
An EST database from Sorghum: ovaries of varying immature stages
Unpublished (2000)
Contact: Cordonnier-Pratt MM

```

Laboratory for Genomics and Bioinformatics  
The University of Georgia, Department of Plant Biology  
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA  
Tel: 706 542 1860  
Fax: 706 583 0210  
Email: mmpratt@uga.edu  
Seq primer: JEN REV  
High quality sequence stop: 463  
POLYA=No.

## FEATURES

source

Location/Qualifiers

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1. 465
/organism="Sorghum bicolor"
/mol_type="mRNA"
/db_xref="taxon:4558"
/clone_lib="Ovary 2 (OV2)"
/note="Organ: Mix of ovaries of varying immature stages
from 8-week-old plants; Vector: pBluescript II from Lambda
Zap II; Site: 1: XhoI; Site 2: EcoRI; The library was made
from poly-A RNA in the cloning vector lambda ZAP II.
Clones to be sequenced were prepared by mass excision."
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## ORIGIN

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Query Match 7.9%; Score 121; DB 4; Length 465;
Best Local Similarity 100.0%; Pred. No. 2.3e-56;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 198 GACCGCTGGGAGTACGGCGCAAGTTAAACTCAAATGAATGACGGGGCCCGCAC 257

Qy 926 AAGCGTGGAGCATGTGTTTAATTCGATGCAACGCGAAGAACCTTACCTGCTTTGACA 985
Db 258 AAGCGTGGAGCATGTGTTTAATTCGATGCAACGCGAAGAACCTTACCTGCTTTGACA 317

Qy 986 T 986
Db 318 T 318
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## RESULT 5

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DEFINITION BACPP33-C16.Y Pristionchus pacificus BAC ends Pristionchus
pacificus genomic, genomic survey sequence.
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ACCESSION BH831257

VERSION BH831257.1 GI:21028759

KEYWORDS GSS.

SOURCE

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ORGANISM Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
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REFERENCE 1 (bases 1 to 473)

SRINIVASAN, J., SINZ, W., LANZ, C., BRAND, A., NANDAKUMAR, R.,  
RADDATZ, G., WITTE, H., KELLER, H., KIPPING, I., PIRES DA SILVA, A.,  
JESSE, T., MILLARE, J., DE BOTH, M., SCHUSTER, S.C. and SOMMER, R.J.  
A BAC-based genetic linkage map of the nematode Pristionchus  
pacificus

TITLE

Unpublished (2002)

## JOURNAL

Evolutionary Biology  
Max-Planck-Institute for Developmental Biology  
Spemannstr. 37-39, Tuebingen D-72076, Germany

Tel: 00497071601371

Fax: 00497071601498

Email: ralf.sommer@tuebingen.mpg.de

Class: BAC ends.

## FEATURES

source

Location/Qualifiers

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1. 473
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/mol_type="genomic DNA"
/strain="var. California"
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## ORIGIN

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Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 223 GACCGCTGGGAGTACGGCGCAAGTTAAACTCAAATGAATGACGGGGCCCGCAC 282

Qy 926 AAGCGTGGAGCATGTGTTTAATTCGATGCAACGCGAAGAACCTTACCTGCTTTGACA 985
Db 283 AAGCGTGGAGCATGTGTTTAATTCGATGCAACGCGAAGAACCTTACCTGCTTTGACA 342

Qy 986 T 986
Db 343 T 343
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## RESULT 6

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LOCUS BH826849 522 bp DNA linear GSS 20-MAY-2002
DEFINITION BACPP24-C20.z Pristionchus pacificus BAC ends Pristionchus
pacificus genomic, genomic survey sequence.
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ACCESSION BH826849

VERSION BH826849.1 GI:21019674

KEYWORDS GSS.

SOURCE

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ORGANISM Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
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REFERENCE 1 (bases 1 to 522)

SRINIVASAN, J., SINZ, W., LANZ, C., BRAND, A., NANDAKUMAR, R.,  
RADDATZ, G., WITTE, H., KELLER, H., KIPPING, I., PIRES DA SILVA, A.,  
JESSE, T., MILLARE, J., DE BOTH, M., SCHUSTER, S.C. and SOMMER, R.J.  
A BAC-based genetic linkage map of the nematode Pristionchus  
pacificus

TITLE

Unpublished (2002)

## JOURNAL

Evolutionary Biology  
Max-Planck-Institute for Developmental Biology  
Spemannstr. 37-39, Tuebingen D-72076, Germany

Tel: 00497071601371

Fax: 00497071601498

Email: ralf.sommer@tuebingen.mpg.de

Class: BAC ends

## FEATURES

source

Location/Qualifiers

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1. 522
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
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## ORIGIN

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Db 220 GACCGCTGGGAGTACGGCGCAAGTTAAACTCAAATGAATGACGGGGCCCGCAC 279

Qy 926 AAGCGTGGAGCATGTGTTTAATTCGATGCAACGCGAAGAACCTTACCTGCTTTGACA 985
Db 280 AAGCGTGGAGCATGTGTTTAATTCGATGCAACGCGAAGAACCTTACCTGCTTTGACA 339

Qy 986 T 986
Db 340 T 340
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## RESULT 7

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BH822044
LOCUS      BH822044          524 bp    DNA    linear    GSS 20-MAY-2002
DEFINITION BACpP17-A15.y Pristionchus pacificus BAC ends Pristionchus
            pacificus genomic, genomic survey sequence.
ACCESSION  BH822044
VERSION    BH822044.1 GI:20998383
KEYWORDS   GSS.
SOURCE     Pristionchus pacificus
            Pristionchus pacificus
            Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
            Neodiplogasteridae; Pristionchus.
REFERENCE  1 (bases 1 to 524)
AUTHORS   Srinivasan,J., Sinz,W., Lanz,C., Brand,A., Nandakumar,R.,
            Raddatz,G., Witte,H., Keller,H., Kipping,I., Pires da Silva,A.,
            Jesse,T., Millare,J., de Both,M., Schuster,S.C. and Sommer,R.U.
TITLE     A BAC-based genetic linkage map of the nematode Pristionchus
            pacificus
JOURNAL   Unpublished (2002)
COMMENT   Contact: Sommer RJ
            Evolutionary Biology
            Max-Planck-Institute for Developmental Biology
            Spemannstr. 37-39, Tuebingen D-72076, Germany
            Tel: 00497071601371
            Fax: 00497071601498
            Email: ralf.sommer@tuebingen.mpg.de
            Class: BAC ends.
            Location/Qualifiers
                1..524
                /organism="Pristionchus pacificus"
                /mol_type="genomic DNA"
                /strain="var. California"
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                /clone_lib="Pristionchus pacificus BAC ends"

ORIGIN
Query Match      7.9%; Score 121; DB 8; Length 524;
Best Local Similarity 100.0%; Pred. No. 2.4e-56;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 866 GACCGCTGGGGAGTACGGCGCAAGGTTAAACTCAATGAATGACGGGGGCGCCGAC 925
      |||||||
DB 223 GACCGCTGGGGAGTACGGCGCAAGGTTAAACTCAATGAATGACGGGGGCGCCGAC 282
      |||||||

QY 926 AAGCGGTGGAGCATGTGTTTAAATCGATCGACGCGAAGACCTTACCTGGTCTTGACA 985
      |||||||
DB 283 AAGCGGTGGAGCATGTGTTTAAATCGATCGACGCGAAGACCTTACCTGGTCTTGACA 342
      |||||||

QY 986 T 986
      |
DB 343 T 343

RESULT 8
CF339295
LOCUS      CF339295          542 bp    mRNA    linear    EST 18-AUG-2003
DEFINITION RCL1--04-G22.g1 Regenerated callus lambda phage cDNA library (RCL1)
            Oryza sativa (japonica cultivar-group) cDNA clone RCL1--04-G22,
            mRNA sequence.
ACCESSION  CF339295
VERSION    CF339295.1 GI:33826975
KEYWORDS   EST.
SOURCE     Oryza sativa (japonica cultivar-group)
            Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE  1 (bases 1 to 542)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
COMMENT   Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

```

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of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
    1..542
    /organism="Oryza sativa (japonica cultivar-group)"
    /mol_type="mRNA"
    /cultivar="Nackdong"
    /db_xref="taxon:39947"
    /clone="RCL1--04-G22"
    /tissue_type="callus"
    /dev_stage="proliferated callus on 2N6 media for 30 days"
    /lab_host="E.coli SOLR"
    /clone_lib="Regenerated callus lambda phage cDNA library (RCL1)"
    /notes="Vector: pBluescript SK(+); Site 1: SstI; Site 2:
            XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
            end with SstI and 3' end with XhoI site. Callus was
            induced on 2N6 media for 30 days and cultured for 36hrs on
            regenerated media"

ORIGIN
Query Match      7.9%; Score 121; DB 7; Length 542;
Best Local Similarity 100.0%; Pred. No. 2.4e-56;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 866 GACCGCTGGGGAGTACGGCGCAAGGTTAAACTCAATGAATGACGGGGGCGCCGAC 925
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DB 259 GACCGCTGGGGAGTACGGCGCAAGGTTAAACTCAATGAATGACGGGGGCGCCGAC 318
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QY 926 AAGCGGTGGAGCATGTGTTTAAATCGATCGACGCGAAGACCTTACCTGGTCTTGACA 985
      |||||||
DB 319 AAGCGGTGGAGCATGTGTTTAAATCGATCGACGCGAAGACCTTACCTGGTCTTGACA 378
      |||||||

QY 986 T 986
      |
DB 379 T 379

RESULT 9
AG019018
LOCUS      AG019018          592 bp    DNA    linear    GSS 09-JAN-2003
DEFINITION Homo sapiens genomic DNA, 21q region, clone: B753B2BB067R, genomic
            survey sequence.
ACCESSION  AG019018
VERSION    AG019018.1 GI:6017504
KEYWORDS   GSS.
SOURCE     Homo sapiens (human)
            Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS   Hattori,M., Fujiyama,A., Ishii,K., Toyoda,A., Taylor,T.,
            Park,H.-S., Yada,T., Watanabe,H. and Sakaki,Y.
TITLE     Homo sapiens genomic DNA, chromosome 21q
JOURNAL   Published Only in Database (1999)
AUTHORS   Hattori,M., Fujiyama,A., Ishii,K., Toyoda,A., Taylor,T.,
            Park,H.-S., Yada,T., Watanabe,H. and Sakaki,Y.
TITLE     Direct Submission
JOURNAL   Submitted (10-OCT-1999) Masahito Hattori, RIKEN Genomic Sciences
            Center(GSC) c/o Kitasato University; 1-15-1 Kitasato, Sagamihara,
            Kanagawa 228-8555, Japan (E-mail:hattori@hgci.ims.u-tokyo.ac.jp,
            Tel:81-42-778-9923, Fax:81-42-778-9924)
            Location/Qualifiers
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                /organism="Homo sapiens"
                /mol_type="genomic DNA"
                /db_xref="taxon:9606"
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/clone="B753B2BB067R"

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Best Local Similarity 100.0%; Pred. No. 2.4e-56;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 866 GACCCCTGGGGAGTACGGCCGCAAGGTTAAACTCAAATGAATGACGGGGCCCGCAC 925
      |||||
Db 174 GACCCCTGGGGAGTACGGCCGCAAGGTTAAACTCAAATGAATGACGGGGCCCGCAC 233

Qy 926 AAGCGGTGGAGCATGTGTTTAATTCGATGCAACCGGAAGACCTTACCTGCTTTGACA 985
      |||||
Db 234 AAGCGGTGGAGCATGTGTTTAATTCGATGCAACCGGAAGACCTTACCTGCTTTGACA 293

Qy 986 T 986
      |
Db 294 T 294

RESULT 10
B0152671
LOCUS B0152671 609 bp mRNA linear EST 24-APR-2002
DEFINITION NF022A12IR1097 Irradiated Medicago truncatula cDNA clone
          NF022A12IR 5', mRNA sequence.
ACCESSION B0152671
VERSION B0152671.1 GI:20289730
KEYWORDS EST.
SOURCE Medicago truncatula (barrel medic)
ORGANISM Medicago truncatula
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
          rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
          Medicago.
REFERENCE 1 (bases 1 to 609)
          Torres-Jerez,I., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J.,
          Flores,H.R., Inman,J.T., Weller,J.W. and May,G.D.
          Expressed Sequence Tags from the Samuel Roberts Noble Foundation
          Medicago truncatula irradiated library
          Unpublished (2001)
          Contact: May GD
          Plant Biology Division
          The Samuel Roberts Noble Foundation
          2510 Sam Noble Parkway, Ardmore, OK 73402, USA
          Tel: 580 224 6650
          Fax: 580 224 6692
          Email: gdmay@noble.org
Insert Length: 609 Std Error: 0.00
Plate: 022 row: A column: 12
Seq primer: TCACACAGGAACAGCTATGAC.
          Location/Qualifiers
            1..609
              /organism="Medicago truncatula"
              /mol_type="mRNA"
              /db_xref="taxon:3880"
              /clone="NF022A12IR"
              /tissue_type="seedlings"
              /dev_stage="seedling"
              /clone_lib="irradiated"
              /note="Vector: Lambda Zap; Seedlings were exposed either
              to 100 Gy gamma or 0.5, 1, 5, or 10 kJ/m2 UV irradiation.
              Gamma-irradiated samples were harvested at 6, 12, 24 and
              48 hours after treatment. UV-irradiated samples were
              harvested 24 hours post-treatment. cDNA was prepared from
              polyA+ enriched, pooled samples of equivalent amounts of
              total RNA from each sample. The cDNA was directionally
              ligated into the Uni-Zap XR vector (Stratagene) and
              packaged using the Gigapack III Gold packaging extracts.
              Phagemids containing cDNA inserts were in vivo excised
              from the recombinant Uni-Zap XR vector using ExAssist
              helper phage and the E. coli strain XL1-Blue MRF'
              (Stratagene). Excised plasmids were plated using SOLR
              cells."
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ORIGIN

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Query Match          7.9%; Score 121; DB 5; Length 609;
Best Local Similarity 100.0%; Pred. No. 2.4e-56;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 866 GACCCCTGGGGAGTACGGCCGCAAGGTTAAACTCAAATGAATGACGGGGCCCGCAC 925
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Db 368 GACCCCTGGGGAGTACGGCCGCAAGGTTAAACTCAAATGAATGACGGGGCCCGCAC 427

Qy 926 AAGCGGTGGAGCATGTGTTTAATTCGATGCAACCGGAAGACCTTACCTGCTTTGACA 985
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Db 428 AAGCGGTGGAGCATGTGTTTAATTCGATGCAACCGGAAGACCTTACCTGCTTTGACA 487

Qy 986 T 986
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Db 488 T 488

RESULT 11
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LOCUS BH818000 639 bp DNA linear GSS 20-MAY-2002
DEFINITION BACPP10-K24.y Pristionchus pacificus BAC ends Pristionchus
          pacificus genomic, genomic survey sequence.
ACCESSION BH818000
VERSION BH818000.1 GI:20989984
KEYWORDS GSS.
SOURCE Pristionchus pacificus
ORGANISM Pristionchus pacificus
          Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
          Neodiplogasteridae; Pristionchus.
REFERENCE 1 (bases 1 to 639)
          Srinivasan,J., Sinz,W., Lanz,C., Brand,A., Nandakumar,R.,
          Raddatz,G., Witte,H., Keller,H., Kipping,I., Pires da Silva,A.,
          Jesse,T., Millare,J., de Both,M., Schuster,S.C. and Sommer,R.J.
          A BAC-based genetic linkage map of the nematode Pristionchus
          pacificus
          Unpublished (2002)
          Contact: Sommer RJ
          Evolutionary Biology
          Max-Planck-Institute for Developmental Biology
          Spemannstr. 37-39, Tuebingen D-72076, Germany
          Tel: 00497071601371
          Fax: 00497071601498
          Email: ralf.sommer@tuebingen.mpg.de
          Class: BAC ends.
          Location/Qualifiers
            1..639
              /organism="Pristionchus pacificus"
              /mol_type="genomic DNA"
              /strain="var. California"
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ORIGIN

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Query Match          7.9%; Score 121; DB 8; Length 639;
Best Local Similarity 100.0%; Pred. No. 2.4e-56;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 866 GACCCCTGGGGAGTACGGCCGCAAGGTTAAACTCAAATGAATGACGGGGCCCGCAC 925
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Qy 926 AAGCGGTGGAGCATGTGTTTAATTCGATGCAACCGGAAGACCTTACCTGCTTTGACA 985
      |||||
Db 280 AAGCGGTGGAGCATGTGTTTAATTCGATGCAACCGGAAGACCTTACCTGCTTTGACA 339

Qy 986 T 986
      |
Db 340 T 340

RESULT 12
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BH822078      BH822078      646 bp      DNA      linear      GSS 20-MAY-2002
LOCUS          BACPPI7-E05.y Pristionchus pacificus BAC ends Pristionchus
DEFINITION     pacificus genomic, genomic survey sequence.
ACCESSION      BH822078
VERSION        BH822078.1 GI:20998480
KEYWORDS       GSS.
SOURCE         Pristionchus pacificus
ORGANISM       Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
REFERENCE      1 (bases 1 to 646)
AUTHORS        Srinivasan,J., Sinz,W., Lanz,C., Brand,A., Nandakumar,R.,
Raddatz,G., Witte,H., Keller,H., Kipping,I., Pires da Silva,A.,
Jesse,T., Millare,J., de Both,M., Schuster,S.C. and Sommer,R.J.
TITLE          A BAC-based genetic linkage map of the nematode Pristionchus
JOURNAL        Unpublished (2002)
COMMENT        Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
Class: BAC ends.

FEATURES             Location/Qualifiers
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                     /organism="Pristionchus pacificus"
                     /mol_type="genomic DNA"
                     /strain="var. California"
                     /db_xref="taxon:54126"
                     /clone_lib="Pristionchus pacificus BAC ends"

ORIGIN
Query Match      7.9%; Score 121; DB 8; Length 646;
Best Local Similarity 100.0%; Pred. No. 2.4e-56;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      866  GACCGCTGGGAGTACGGCGCAAGGTTAAACTCAAACTCAATGAATTCACGGGGCCGCAC 925
Db      223  GACCGCTGGGAGTACGGCGCAAGGTTAAACTCAAACTCAATGAATTCACGGGGCCGCAC 282
Qy      926  AAGCGGTGGAGCATGTGGTTTAATTCGATGCAACGCGAAGACCTTACCTGGTCTTGACA 985
Db      283  AAGCGGTGGAGCATGTGGTTTAATTCGATGCAACGCGAAGACCTTACCTGGTCTTGACA 342
Qy      986  T 986
Db      343  T 343

RESULT 14
CF339842
LOCUS          CF339842
DEFINITION     RCL1--06-B12.g1 Regenerated callus lambda phage cDNA library (RCL1)
Oryza sativa (japonica cultivar-group) cDNA clone RCL1--06-B12,
mRNA sequence.
ACCESSION      CF339842.1 GI:33828055
VERSION        CF339842
KEYWORDS       EST.
SOURCE         Oryza sativa (japonica cultivar-group)
ORGANISM       Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE      1 (bases 1 to 658)
AUTHORS        Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE          Large-scale Sequencing Analysis of Rice ESTs
JOURNAL        Unpublished (2003)
COMMENT        Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /cultivar="Nackdong"
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                     /clone="RCL1--06-B12"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli SOLR"
                     /clone_lib="Regenerated callus lambda phage cDNA library
(RCL1)"
                     /note="Vector: pBluescript SK(+); Site_1: SstI; Site_2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with SstI and 3' end with XhoI site. Callus was

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BH822078      BH822078      646 bp      DNA      linear      GSS 20-MAY-2002
LOCUS          BACPPI7-E05.y Pristionchus pacificus BAC ends Pristionchus
DEFINITION     pacificus genomic, genomic survey sequence.
ACCESSION      BH822078
VERSION        BH822078.1 GI:20998480
KEYWORDS       GSS.
SOURCE         Pristionchus pacificus
ORGANISM       Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
REFERENCE      1 (bases 1 to 646)
AUTHORS        Srinivasan,J., Sinz,W., Lanz,C., Brand,A., Nandakumar,R.,
Raddatz,G., Witte,H., Keller,H., Kipping,I., Pires da Silva,A.,
Jesse,T., Millare,J., de Both,M., Schuster,S.C. and Sommer,R.J.
TITLE          A BAC-based genetic linkage map of the nematode Pristionchus
JOURNAL        Unpublished (2002)
COMMENT        Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
Class: BAC ends.

FEATURES             Location/Qualifiers
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                     /mol_type="genomic DNA"
                     /strain="var. California"
                     /db_xref="taxon:54126"
                     /clone_lib="Pristionchus pacificus BAC ends"

ORIGIN
Query Match      7.9%; Score 121; DB 8; Length 646;
Best Local Similarity 100.0%; Pred. No. 2.4e-56;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      866  GACCGCTGGGAGTACGGCGCAAGGTTAAACTCAAACTCAATGAATTCACGGGGCCGCAC 925
Db      223  GACCGCTGGGAGTACGGCGCAAGGTTAAACTCAAACTCAATGAATTCACGGGGCCGCAC 282
Qy      926  AAGCGGTGGAGCATGTGGTTTAATTCGATGCAACGCGAAGACCTTACCTGGTCTTGACA 985
Db      283  AAGCGGTGGAGCATGTGGTTTAATTCGATGCAACGCGAAGACCTTACCTGGTCTTGACA 342
Qy      986  T 986
Db      343  T 343

RESULT 13
BH833826
LOCUS          BH833826
DEFINITION     BACPPE-P05.y Pristionchus pacificus BAC ends Pristionchus
genomic, genomic survey sequence.
ACCESSION      BH833826
VERSION        BH833826.1 GI:21034053
KEYWORDS       GSS.
SOURCE         Pristionchus pacificus
ORGANISM       Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
REFERENCE      1 (bases 1 to 646)
AUTHORS        Srinivasan,J., Sinz,W., Lanz,C., Brand,A., Nandakumar,R.,
Raddatz,G., Witte,H., Keller,H., Kipping,I., Pires da Silva,A.,
Jesse,T., Millare,J., de Both,M., Schuster,S.C. and Sommer,R.J.
TITLE          A BAC-based genetic linkage map of the nematode Pristionchus
JOURNAL        Unpublished (2002)
COMMENT        Contact: Sommer RJ
Evolutionary Biology

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Search completed: April 12, 2005, 14:24:54  
Job time : 5298 secs

	Query Match	7.9%;	Score 121;	DB 7;	Length 658;
	Best Local Similarity	100.0%;	Pred. No. 2.4e-56;		
	Matches 121;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
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Db	258	GACCGCTGGGGAGTACGGCCGCAAGTTAAAACTCAAATGAATTCACGGGGGCCCGCAC	317		
QY	926	AAGCGGTGGAGCATGTGGTTTAAATTCGATGCACACGGCGAAGCACTTACCTGGTCTTTGACA	985		
Db	318	AAGCGGTGGAGCATGTGGTTTAAATTCGATGCACACGGCGAAGCACTTACCTGGTCTTTGACA	377		
QY	986	T 986			
Db	378	T 378			

RESULT 15	BH820342	linear	GSS 20-MAY-2002
LOCUS	BACPP14-004.y	Pristionchus pacificus	BAC ends Pristionchus
DEFINITION		genomic, genomic survey sequence.	
ACCESSION	BH820342		
VERSION	BH820342.1	GI:20995245	
KEYWORDS		GSS.	
SOURCE		Pristionchus pacificus	
ORGANISM		Pristionchus pacificus	
		Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;	
REFERENCE		Neodiplogasteridae; Pristionchus.	
AUTHORS		1 (bases 1 to 661)	
		Srinivasan,J., Sinz,W., Lanz,C., Brand,A., Nandakumar,R.,	
		Raddatz,G., Witte,H., Keller,H., Kipping,I., Pires da Silva,A.,	
		Jesse,T., Millare,J., de Boch,M., Schuster,S.C. and Sommer,R.J.	
TITLE		A BAC-based genetic linkage map of the nematode Pristionchus	
JOURNAL		pacificus	
COMMENT		Unpublished (2002)	
		Contact: Sommer RJ	
		Evolutionary Biology	
		Max-Planck-Institute for Developmental Biology	
		Spenannstr. 37-39, Tuebingen D-72076, Germany	
		Tel: 00497071601371	
		Fax: 00497071601498	
		Email: ralf.sommer@tuebingen.mpg.de	
		Class: BAC ends.	

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Class: LAC ends:
Location/Qualifiers
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/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="var. California"
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FEATURES
source

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ORIGIN		7.9%; Score 121; DB 8; Length 661;	
Query Match		Best Local Similarity 100.0%; Pred. No. 2.4e-56;	
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	866	GACCGCTGGGAGTACGGCCGAAGTTTAAACTCAAATGAATTGACGGGGGCCCGCAC	925
Ddb	223	GACCGCTGGGAGTACGGCCGAAGTTTAAACTCAAATGAATTGACGGGGGCCCGCAC	282
Qy	926	AAGCGGTGGAGCATGTGGTTTAAATTCGATGCACACGGAGAAGCTTACCTGGTCTTTGACA	985
Ddb	283	AAGCGGTGGAGCATGTGGTTTAAATTCGATGCACACGGAGAAGCTTACCTGGTCTTTGACA	342
Qy	986	T 986	
Ddb	343	T 343	

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Result	No.	Score	Query		DB	ID	Description
			Match	Length			
C	1	19	100.0	19	6	E58428	DNA probe f
	2	19	100.0	193	1	AJ842303	unidentif
	3	19	100.0	194	1	AJ842302	unidentif
C	4	19	100.0	300	1	AF025555	Psychroba
	5	19	100.0	1403	1	AB094456	Psychroba
	6	19	100.0	1462	1	AB094458	Psychroba
	7	19	100.0	1473	1	PSP51093	Psychroba
	8	19	100.0	1473	1	PSP51098	Psychroba
	9	19	100.0	1473	1	PSP551101	Psychroba
	10	19	100.0	1520	1	AB016059	Psychroba
	11	19	100.0	1525	1	AB016056	Psychroba
	12	19	100.0	1526	1	AB016057	Psychroba
	13	19	100.0	1526	6	E58427	DNA probe f
	14	19	100.0	1530	1	AB016058	Psychroba
	15	19	100.0	1531	1	AB016055	Psychroba
	16	19	100.0	1536	1	AB016054	Psychroba
	17	19	100.0	1684	1	PSP551107	Psychroba
	18	17.4	91.6	161	1	AF440839	Unculture
	19	17.4	91.6	165	1	AF440847	Unculture

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RESULT 2
AJ842303/c
LOCUS      AJ842303                193 bp    DNA        linear    BCT 12-OCT-2004
DEFINITION unidentified bacterium partial 16S rRNA gene, clone SD33.
ACCESSION  AJ842303
VERSION     AJ842303.1 GI:52839363
KEYWORDS   16S ribosomal RNA; 16S rRNA gene.
SOURCE     unidentified bacterium
ORGANISM   Bacteria; environmental samples.
REFERENCE  1
AUTHORS    Li, M.
TITLE      A survey of microbial diversity around the Chinese Antarctic
JOURNAL    Research Station and its environmental significance
REFERENCE  2 (bases 1 to 193)
AUTHORS    Li, M.
TITLE      Direct Submission
JOURNAL    Submitted (08-SEP-2004) Li M., Marine Biogenetic Resource
          Laboratory, Third Institute of Oceanography, SOA, 184 Daxue Road,
          Xiamen, Fujian Province, 361005, CHINA
FEATURES   Location/Qualifiers
            source
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Best Local Similarity 100.0%; Pred. No. 47;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1  CCCGGGGGACGATGACATTA 19
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Db  66  CCCGGGGGACGATGACATTA 48

RESULT 3
AJ842302/c
LOCUS      AJ842302                194 bp    DNA        linear    BCT 12-OCT-2004
DEFINITION unidentified bacterium partial 16S rRNA gene, clone SD32.
ACCESSION  AJ842302
VERSION     AJ842302.1 GI:52839362
KEYWORDS   16S ribosomal RNA; 16S rRNA gene.
SOURCE     unidentified bacterium
ORGANISM   Bacteria; environmental samples.
REFERENCE  1
AUTHORS    Li, M.
TITLE      A survey of microbial diversity around the Chinese Antarctic
JOURNAL    Research Station and its environmental significance
REFERENCE  2 (bases 1 to 194)
AUTHORS    Li, M.
TITLE      Direct Submission
JOURNAL    Submitted (08-SEP-2004) Li M., Marine Biogenetic Resource
          Laboratory, Third Institute of Oceanography, SOA, 184 Daxue Road,
          Xiamen, Fujian Province, 361005, CHINA
FEATURES   Location/Qualifiers
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              /mol_type="genomic DNA"
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Best Local Similarity 100.0%; Pred. No. 47;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1  CCCGGGGGACGATGACATTA 19
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Db  66  CCCGGGGGACGATGACATTA 48

RESULT 4
AF025555
LOCUS      AF025555                300 bp    DNA        linear    BCT 11-SEP-2000
DEFINITION Psychrobacter glacincola 16S ribosomal RNA gene, partial sequence.
ACCESSION  AF025555
VERSION     AF025555.1 GI:2582456
KEYWORDS   Psychrobacter glacincola
SOURCE     Psychrobacter glacincola
           Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
           Moraxellaceae; Psychrobacter.
REFERENCE  1 (bases 1 to 300)
AUTHORS    Hagstrom, A., Pinhassi, J. and Zweifel, U. L.
TITLE      Biogeographical diversity among marine bacterioplankton
JOURNAL    Aquat. Microb. Ecol. 21, 231-244 (2000)
REFERENCE  2 (bases 1 to 300)
AUTHORS    Pinhassi, J., Zweifel, U. L. and Hagstrom, A.
TITLE      Direct Submission
JOURNAL    Submitted (18-SEP-1997) National Environmental Research Institute,
           Frederiksbergvej 399, Roskilde DK-4000, Denmark
FEATURES   Location/Qualifiers
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              /mol_type="genomic DNA"
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              /db_xref="taxon:56810"
              /note="isolated from the NW Mediterranean"
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Best Local Similarity 100.0%; Pred. No. 47;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1  CCCGGGGGACGATGACATTA 19
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Db  250  CCCGGGGGACGATGACATTA 268

RESULT 5
AB094456
LOCUS      AB094456                1403 bp    DNA        linear    BCT 11-DEC-2003
DEFINITION Psychrobacter sp. MJYP.15.12 gene for 16S rRNA, partial sequence.
ACCESSION  AB094456
VERSION     AB094456.1 GI:27807566
KEYWORDS   Psychrobacter sp. MJYP.15.12
SOURCE     Psychrobacter sp. MJYP.15.12
ORGANISM   Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
           Moraxellaceae; Psychrobacter.
REFERENCE  1
AUTHORS    Inagaki, F., Suzuki, M., Takai, K., Oida, H., Sakamoto, T., Aoki, K.,
           Nealson, K. H. and Horikoshi, K.
TITLE      Microbial Communities Associated with Geological Horizons in
           Coastal Seafloor Sediments from the Sea of Okhotsk

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JOURNAL      Appl. Environ. Microbiol. 69 (12), 7224-7235 (2003)
PUBMED       14660370
REFERENCE     2 (bases 1 to 1403)
AUTHORS      Inagaki, F.
TITLE        Direct Submission
JOURNAL      Submitted (23-OCT-2002) Fumio Inagaki, Japan Marine Science &
              Technology Center, Subground Animalcule Retrieval (SUGAR) Project,
              Frontier Research System for Extremophiles; Natsuchima-cho 2-15,
              Yokosuka 237-0061, Japan (E-mail: inagaki@jamstec.go.jp,
              Tel: 81-468-67-9687, Fax: 81-468-67-9715)
FEATURES     Location/Qualifiers
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                /mol_type="genomic DNA"
                /strain="MJYP.15.12"
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source
rRNA
ORIGIN
Query Match      100.0%; Score 19; DB 1; Length 1403;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCGGGACGATGACATTA 19
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Db 440 CCCGGGACGATGACATTA 458

RESULT 6
AB094458
LOCUS       AB094458                1462 bp    DNA    linear    BCT 11-DEC-2003
DEFINITION  Psychrobacter sp. MJYP.25.32 gene for 16S rRNA, partial sequence.
ACCESSION   AB094458
VERSION     AB094458.1 GI:27807568
KEYWORDS
SOURCE      Psychrobacter sp. MJYP.25.32
            Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
            Moraxellaceae; Psychrobacter.
REFERENCE   1
AUTHORS     Inagaki, F., Suzuki, M., Takai, K., Oida, H., Sakamoto, T., Aoki, K.,
              Neelson, K.H. and Horikoshi, K.
TITLE       Microbial Communities Associated with Geological Horizons in
              Coastal Subseafloor Sediments from the Sea of Okhotsk
JOURNAL     Appl. Environ. Microbiol. 69 (12), 7224-7235 (2003)
PUBMED     14660370
REFERENCE   2 (bases 1 to 1462)
AUTHORS     Inagaki, F.
TITLE       Direct Submission
JOURNAL     Submitted (23-OCT-2002) Fumio Inagaki, Japan Marine Science &
              Technology Center, Subground Animalcule Retrieval (SUGAR) Project,
              Frontier Research System for Extremophiles; Natsuchima-cho 2-15,
              Yokosuka 237-0061, Japan (E-mail: inagaki@jamstec.go.jp,
              Tel: 81-468-67-9687, Fax: 81-468-67-9715)
FEATURES     Location/Qualifiers
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source
rRNA
ORIGIN
Query Match      100.0%; Score 19; DB 1; Length 1462;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCGGGACGATGACATTA 19
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Db 438 CCCGGGACGATGACATTA 456

RESULT 7
PSP551093
LOCUS       PSP551093                1473 bp    DNA    linear    BCT 17-MAY-2004
DEFINITION  Psychrobacter sp. wp8 partial 16S rRNA gene, isolate wp8.
ACCESSION   AJ551093
VERSION     AJ551093.1 GI:34525808
KEYWORDS    16S ribosomal RNA; 16S rRNA gene.
SOURCE      Psychrobacter sp. wp8
            Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
            Moraxellaceae; Psychrobacter.
REFERENCE   1
AUTHORS     Wang, F., Wang, P., Chen, M. and Xiao, X.
TITLE       Isolation of extremophiles with the detection and retrieval of
              Shewanella strains in deep-sea sediments from the west Pacific
              Extremophiles 8 (2), 165-168 (2004)
JOURNAL     Extremophiles 8 (2), 165-168 (2004)
PUBMED     15064982
REFERENCE   2 (bases 1 to 1473)
AUTHORS     Xiao, X.
TITLE       Direct Submission
JOURNAL     Submitted (22-FEB-2003) Xiao X., Key Lab of Marine Biogenetic
              Resources, Third Institute of Oceanography, SOA, Daxuelu 178,
              Xiamen, 361005, CHINA
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rRNA
ORIGIN
Query Match      100.0%; Score 19; DB 1; Length 1473;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCGGGACGATGACATTA 19
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Db 458 CCCGGGACGATGACATTA 476

RESULT 8
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LOCUS       PSP551098                1473 bp    DNA    linear    BCT 17-MAY-2004
DEFINITION  Psychrobacter sp. wp18 partial 16S rRNA gene, isolate wp18.
ACCESSION   AJ551098
VERSION     AJ551098.1 GI:34525813
KEYWORDS    16S ribosomal RNA; 16S rRNA gene.
SOURCE      Psychrobacter sp. wp18
            Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
            Moraxellaceae; Psychrobacter.
REFERENCE   1
AUTHORS     Wang, F., Wang, P., Chen, M. and Xiao, X.
TITLE       Isolation of extremophiles with the detection and retrieval of
              Shewanella strains in deep-sea sediments from the west Pacific
              Extremophiles 8 (2), 165-168 (2004)
JOURNAL     Extremophiles 8 (2), 165-168 (2004)
PUBMED     15064982
REFERENCE   2 (bases 1 to 1473)
AUTHORS     Xiao, X.
TITLE       Direct Submission
JOURNAL     Submitted (22-FEB-2003) Xiao X., Key Lab of Marine Biogenetic
              Resources, Third Institute of Oceanography, SOA, Daxuelu 178,
              Xiamen, 361005, CHINA

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FEATURES	source	Location/Qualifiers	1520 bp	DNA	linear	BCT 10-MAY-2000
LOCUS	AB016059	Psychrobacter pacificensis DNA for 16S rRNA, partial sequence, strain:NIBH P2K18.				
DEFINITION	AB016059	Psychrobacter pacificensis DNA for 16S rRNA, partial sequence, strain:NIBH P2K18.				
ACCESSION	AB016059	Psychrobacter pacificensis DNA for 16S rRNA, partial sequence, strain:NIBH P2K18.				
VERSION	AB016059.1	GI:6691640				
KEYWORDS	16S ribosomal RNA.					
SOURCE	Psychrobacter pacificensis					
ORGANISM	Psychrobacter pacificensis					
REFERENCE	1 (sites)	Moraxellaceae; Psychrobacter.				
AUTHORS	Mariyama,A., Honda,D., Yamamoto,H., Kitamura,K. and Higashihara,T.					
TITLE	Phylogenetic analysis of psychrophilic bacteria isolated from the Japan Trench, including a description of the deep-sea species Psychrobacter pacificensis sp. nov					
JOURNAL	Int. J. Syst. Evol. Microbiol. 50 Pt 2, 835-846 (2000)					
MEDLINE	20222194					
PUBMED	10758895					
REFERENCE	2 (bases 1 to 1520)					
AUTHORS	Mariyama,A. and Kitamura,K.					
TITLE	Direct Submission					
JOURNAL	Submitted (07-JUL-1998) Akihiko Mariyama, National Institute of Bioscience and Human-Technology, Department of Applied and Environmental Microbiology; 1-1 Higashi, Tsukuba, Ibaraki 305-8566, Japan (E-mail:mariyama@nibh.go.jp, Tel:+81-298-54-6062, Fax:+81-298-54-6412)					
FEATURES	source	Location/Qualifiers				
LOCUS	AB016056	Psychrobacter pacificensis DNA for 16S rRNA, partial sequence, strain:NIBH P2J13.				
DEFINITION	AB016056	Psychrobacter pacificensis DNA for 16S rRNA, partial sequence, strain:NIBH P2J13.				
ACCESSION	AB016056	Psychrobacter pacificensis DNA for 16S rRNA, partial sequence, strain:NIBH P2J13.				
VERSION	AB016056.1	GI:6691637				
KEYWORDS	16S ribosomal RNA.					
SOURCE	Psychrobacter pacificensis					
ORGANISM	Psychrobacter pacificensis					
REFERENCE	1 (sites)	Moraxellaceae; Psychrobacter.				
AUTHORS	Mariyama,A., Honda,D., Yamamoto,H., Kitamura,K. and Higashihara,T.					
TITLE	Phylogenetic analysis of psychrophilic bacteria isolated from the Japan Trench, including a description of the deep-sea species Psychrobacter pacificensis sp. nov					
JOURNAL	Int. J. Syst. Evol. Microbiol. 50 Pt 2, 835-846 (2000)					
MEDLINE	20222194					
PUBMED	10758895					
REFERENCE	2 (bases 1 to 1525)					
AUTHORS	Mariyama,A. and Kitamura,K.					
TITLE	Direct Submission					
JOURNAL	Submitted (07-JUL-1998) Akihiko Mariyama, National Institute of Bioscience and Human-Technology, Department of Applied and Environmental Microbiology; 1-1 Higashi, Tsukuba, Ibaraki 305-8566, Japan (E-mail:mariyama@nibh.go.jp, Tel:+81-298-54-6062, Fax:+81-298-54-6412)					
FEATURES	source	Location/Qualifiers				
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DEFINITION	AB016056	Psychrobacter pacificensis DNA for 16S rRNA, partial sequence, strain:NIBH P2J13.				
ACCESSION	AB016056	Psychrobacter pacificensis DNA for 16S rRNA, partial sequence, strain:NIBH P2J13.				
VERSION	AB016056.1	GI:6691637				
KEYWORDS	16S ribosomal RNA.					
SOURCE	Psychrobacter pacificensis					
ORGANISM	Psychrobacter pacificensis					
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AUTHORS	Mariyama,A., Honda,D., Yamamoto,H., Kitamura,K. and Higashihara,T.					
TITLE	Phylogenetic analysis of psychrophilic bacteria isolated from the Japan Trench, including a description of the deep-sea species Psychrobacter pacificensis sp. nov					
JOURNAL	Int. J. Syst. Evol. Microbiol. 50 Pt 2, 835-846 (2000)					
MEDLINE	20222194					
PUBMED	10758895					
REFERENCE	2 (bases 1 to 1525)					
AUTHORS	Mariyama,A. and Kitamura,K.					
TITLE	Direct Submission					
JOURNAL	Submitted (07-JUL-1998) Akihiko Mariyama, National Institute of Bioscience and Human-Technology, Department of Applied and Environmental Microbiology; 1-1 Higashi, Tsukuba, Ibaraki 305-8566, Japan (E-mail:mariyama@nibh.go.jp, Tel:+81-298-54-6062, Fax:+81-298-54-6412)					
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VERSION	AB016056.1	GI:6691637				
KEYWORDS	16S ribosomal RNA.					
SOURCE	Psychrobacter pacificensis					
ORGANISM	Psychrobacter pacificensis					
REFERENCE	1 (sites)	Moraxellaceae; Psychrobacter.				
AUTHORS	Mariyama,A., Honda,D., Yamamoto,H., Kitamura,K. and Higashihara,T.					
TITLE	Phylogenetic analysis of psychrophilic bacteria isolated from the Japan Trench, including a description of the deep-sea species Psychrobacter pacificensis sp. nov					
JOURNAL	Int. J. Syst. Evol. Microbiol. 50 Pt 2, 835-846 (2000)					
MEDLINE	20222194					
PUBMED	10758895					
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Qy 1 CCGGGGACGATGACATTA 19
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RESULT 12
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LOCUS      1526 bp      DNA      linear      BCT 10-MAY-2000
DEFINITION Psychrobacter pacificensis DNA for 16S rRNA, partial sequence,
            strain:NIBH P2K6(T) (=IFO 16279(T)).
ACCESSION AB016057.1 GI:6691638
VERSION    16S ribosomal RNA.
KEYWORDS   Psychrobacter pacificensis
SOURCE     Psychrobacter pacificensis
ORGANISM   Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
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REFERENCE
  AUTHORS   Maruyama,A., Honda,D., Yamamoto,H., Kitamura,K. and Higashihara,T.
  TITLE     Phylogenetic analysis of psychrophilic bacteria isolated from the
            Japan Trench, including a description of the deep-sea species
            Psychrobacter pacificensis sp. nov
  JOURNAL   Int. J. Syst. Evol. Microbiol. 50 Pt 2, 835-846 (2000)
  MEDLINE   2022194
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REFERENCE
  AUTHORS   Maruyama,A. and Kitamura,K.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-JUL-1998) Akihiko Maruyama, National Institute of
            Bioscience and Human-Technology, Department of Applied and
            Environmental Microbiology; 1-1 Higashi, Tsukuba, Ibaraki 305-8566,
            Japan (E-mail:maruyama@nibh.go.jp, Tel: +81-298-54-6062,
            Fax: +81-298-54-6412)
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Db 458 CCGGGGACGATGACATTA 476
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DEFINITION DNA probe for detecting novel psychrophile.
ACCESSION E58427
VERSION    16S ribosomal RNA.
KEYWORDS   Psychrobacter pacificensis
SOURCE     Psychrobacter pacificensis
ORGANISM   Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
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REFERENCE
  AUTHORS   Maruyama,A., Honda,D., Yamamoto,H., Kitamura,K. and Higashihara,T.
  TITLE     Phylogenetic analysis of psychrophilic bacteria isolated from the
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            Psychrobacter pacificensis sp. nov
  JOURNAL   Int. J. Syst. Evol. Microbiol. 50 Pt 2, 835-846 (2000)
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  PUBMED    10758895
REFERENCE
  AUTHORS   Maruyama,A. and Kitamura,K.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-JUL-1998) Akihiko Maruyama, National Institute of
            Bioscience and Human-Technology, Department of Applied and
            Environmental Microbiology; 1-1 Higashi, Tsukuba, Ibaraki 305-8566,
            Japan (E-mail:maruyama@nibh.go.jp, Tel: +81-298-54-6062,
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    |||||
Db 458 CCGGGGACGATGACATTA 476
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DEFINITION DNA probe for detecting novel psychrophile.
ACCESSION E58427
VERSION    16S ribosomal RNA.
KEYWORDS   Psychrobacter pacificensis
SOURCE     Psychrobacter pacificensis
ORGANISM   Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
            Moraxellaceae; Psychrobacter.
REFERENCE
  AUTHORS   Maruyama,A., Honda,D., Yamamoto,H., Kitamura,K. and Higashihara,T.
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            Psychrobacter pacificensis sp. nov
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  PUBMED    10758895
REFERENCE
  AUTHORS   Maruyama,A. and Kitamura,K.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-JUL-1998) Akihiko Maruyama, National Institute of
            Bioscience and Human-Technology, Department of Applied and
            Environmental Microbiology; 1-1 Higashi, Tsukuba, Ibaraki 305-8566,
            Japan (E-mail:maruyama@nibh.go.jp, Tel: +81-298-54-6062,
            Fax: +81-298-54-6412)
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    Maruyama,A., Kitamura,K. and Kurane,R.
  AUTHORS   DNA probe for detecting novel psychrophile
  TITLE     Patent: JP 2000333680-A 1 05-DEC-2000;
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            PI AKIHIKO MARYAMA,KEIKO KITAMURA,RYUICHIRO KURANE PC
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Db 458 CCGGGGACGATGACATTA 476
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DEFINITION Psychrobacter pacificensis DNA for 16S rRNA, partial sequence,
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ACCESSION AB016058.1 GI:6691639
VERSION    16S ribosomal RNA.
KEYWORDS   Psychrobacter pacificensis
SOURCE     Psychrobacter pacificensis
ORGANISM   Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
            Moraxellaceae; Psychrobacter.
REFERENCE
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  AUTHORS   Maruyama,A., Honda,D., Yamamoto,H., Kitamura,K. and Higashihara,T.
  TITLE     Phylogenetic analysis of psychrophilic bacteria isolated from the
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            Psychrobacter pacificensis sp. nov
  JOURNAL   Int. J. Syst. Evol. Microbiol. 50 Pt 2, 835-846 (2000)
  MEDLINE   2022194
  PUBMED    10758895
REFERENCE
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  AUTHORS   Maruyama,A. and Kitamura,K.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-JUL-1998) Akihiko Maruyama, National Institute of
            Bioscience and Human-Technology, Department of Applied and
            Environmental Microbiology; 1-1 Higashi, Tsukuba, Ibaraki 305-8566,
            Japan (E-mail:maruyama@nibh.go.jp, Tel: +81-298-54-6062,
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ORIGIN

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REFERENCE 1 (sites)  
AUTHORS Maruyama A., Honda D., Yamamoto H., Kitamura K. and Higashihara T.  
TITLE Phylogenetic analysis of psychrophilic bacteria isolated from the  
Japan Trench, including a description of the deep-sea species  
Psychrobacter pacificensis sp. nov  
JOURNAL Int. J. Syst. Evol. Microbiol. 50 Pt 2, 835-846 (2000)  
MEDLINE 2022194  
PUBMED 10758895  
REFERENCE 2 (bases 1 to 1531)  
AUTHORS Maruyama A. and Kitamura K.  
TITLE Direct Submission  
JOURNAL Submitted (07-JUL-1998) Akihiko Maruyama, National Institute of  
Bioscience and Human-Technology, Department of Applied and  
Environmental Microbiology; 1-1 Higashi, Tsukuba, Ibaraki 305-8566,  
Japan (E-mail:maruyama@nibh.go.jp, Tel:+81-298-54-6062,  
Fax:+81-298-54-6412)

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## ORIGIN

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